

Figure 1A - (1)

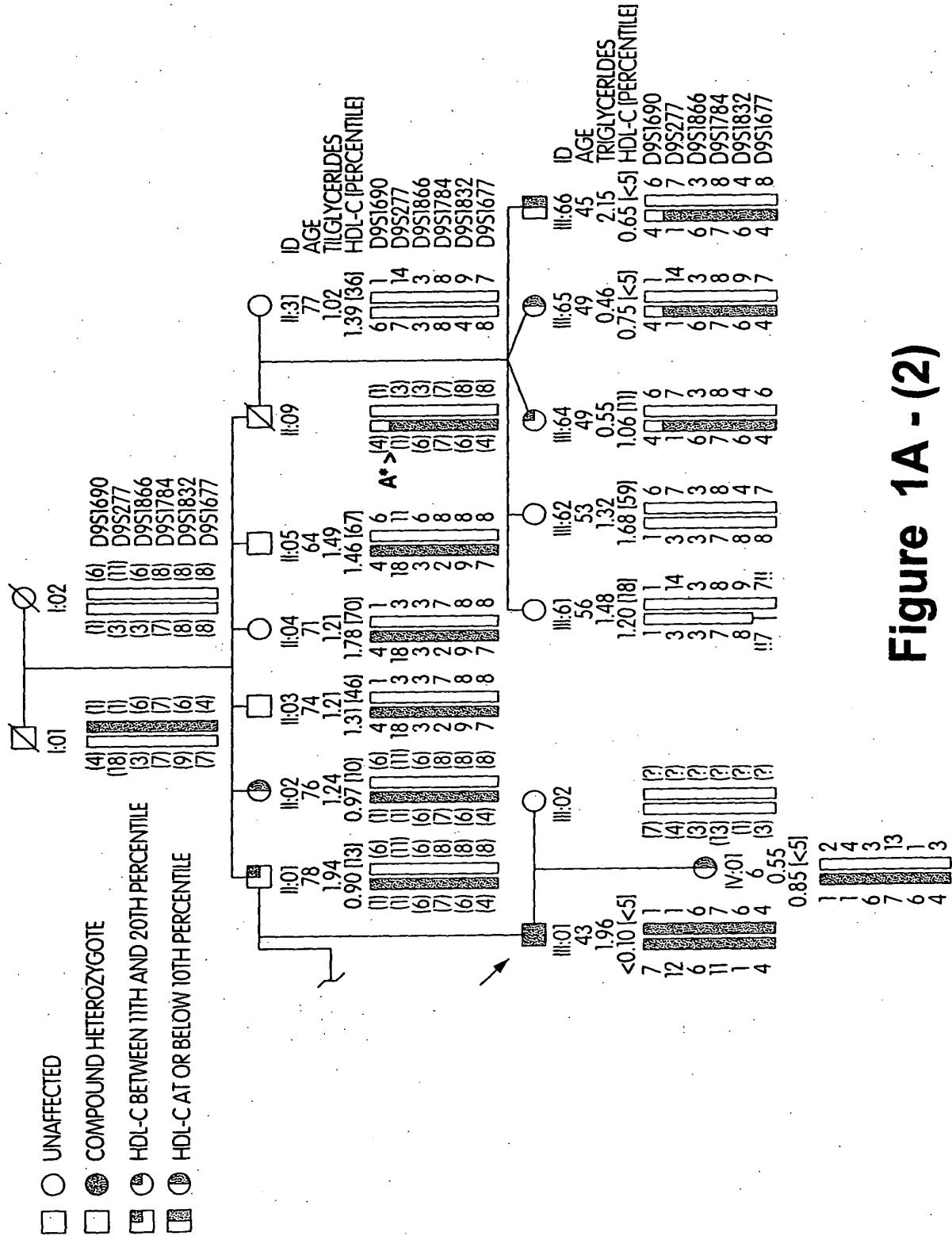


Figure 1A - (2)

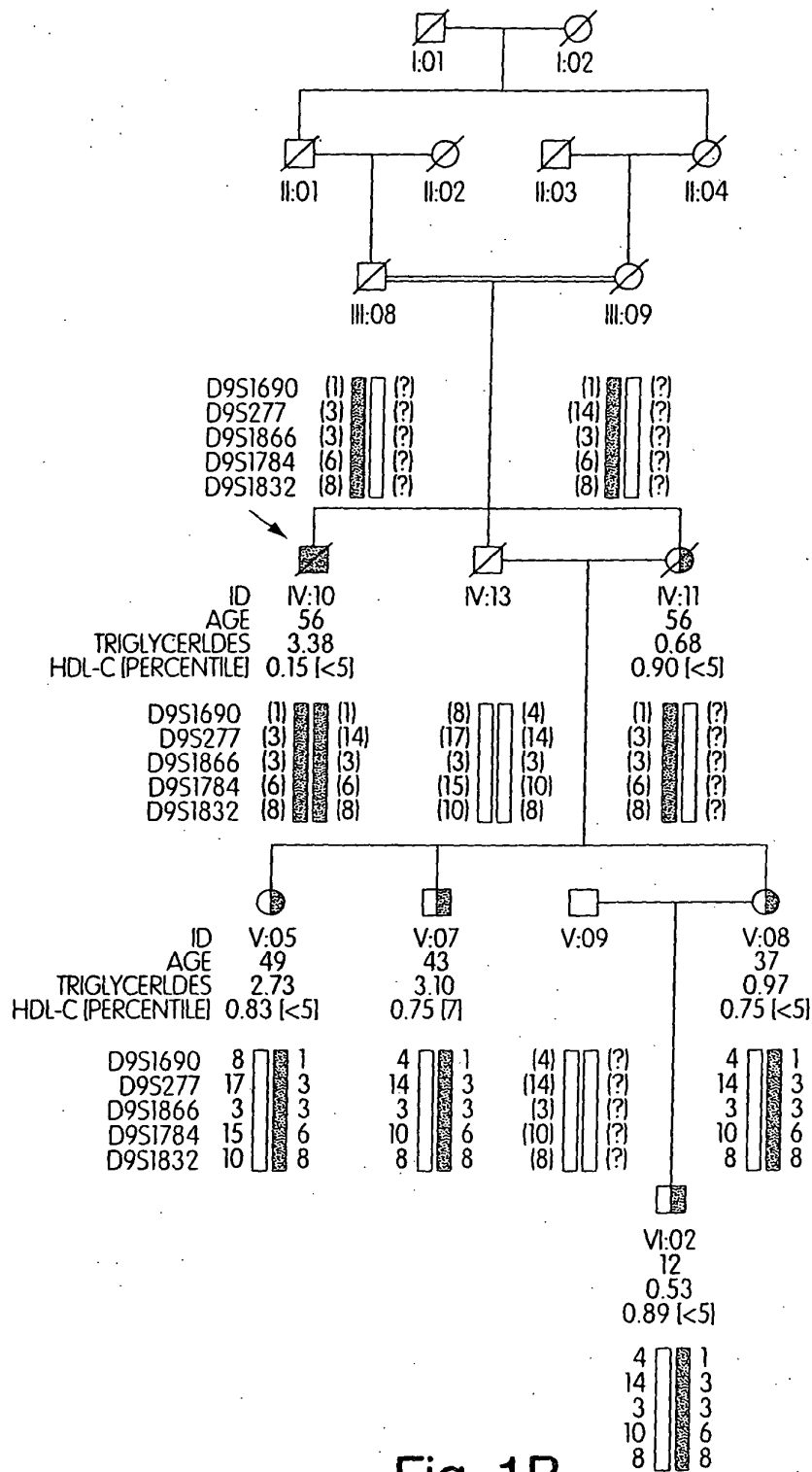


Fig. 1B

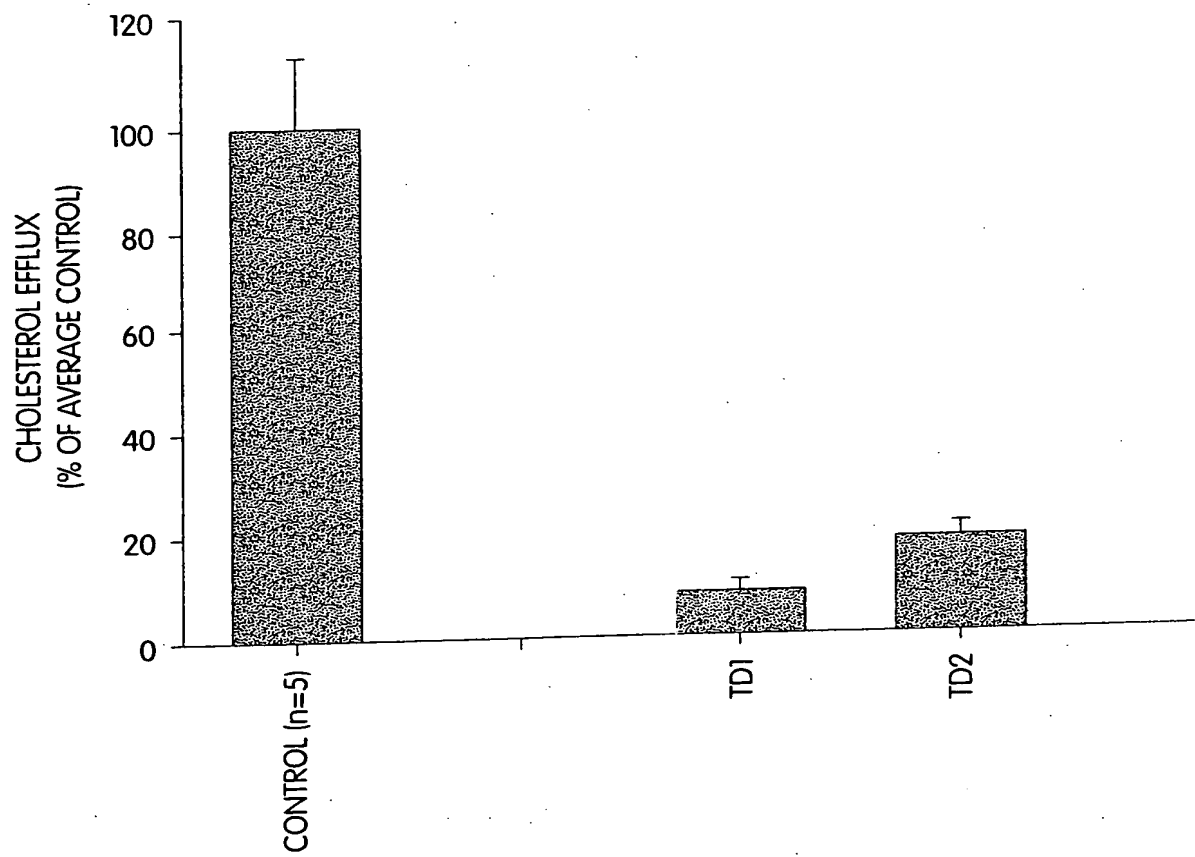


Fig. 1C

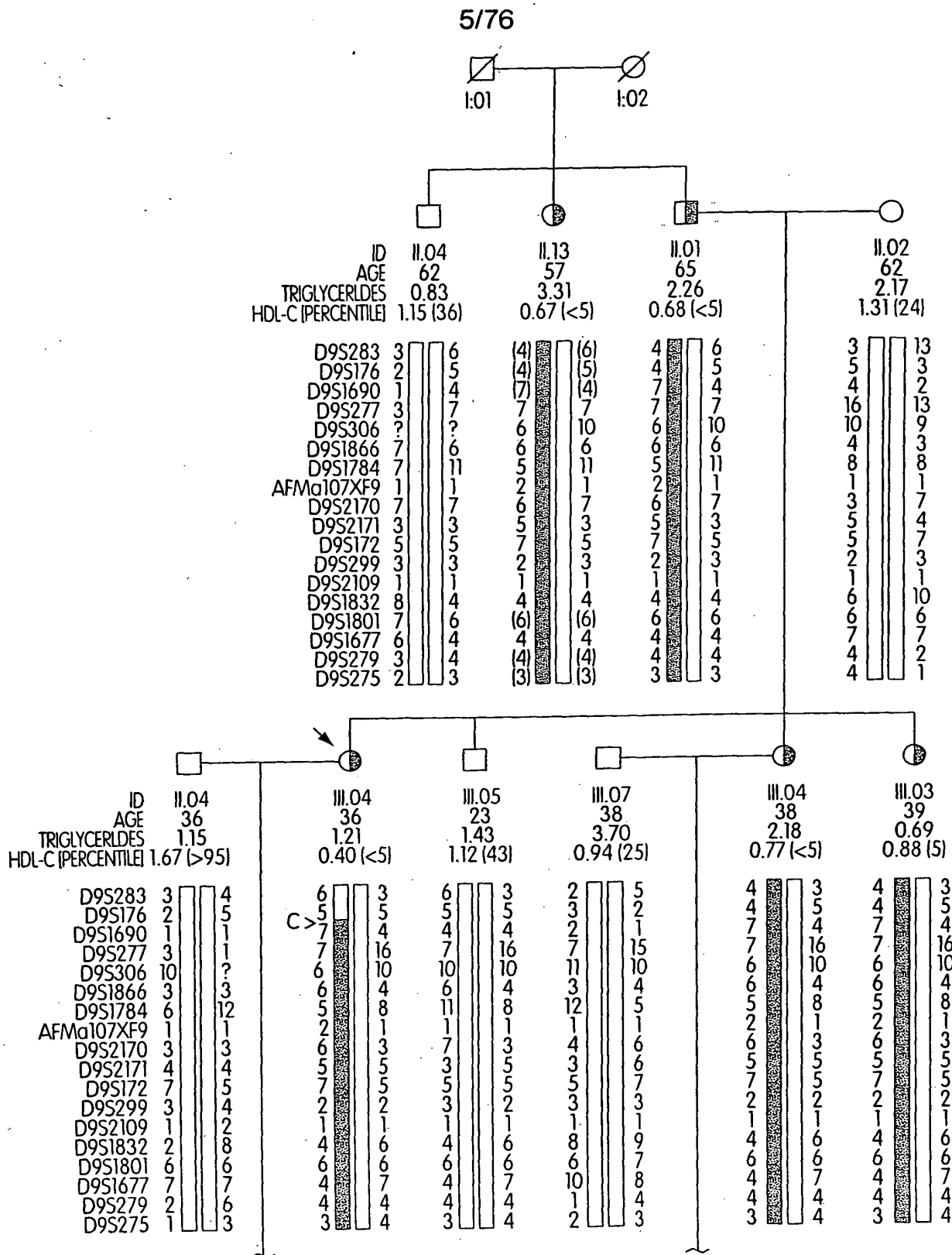


Figure 2A – (1)

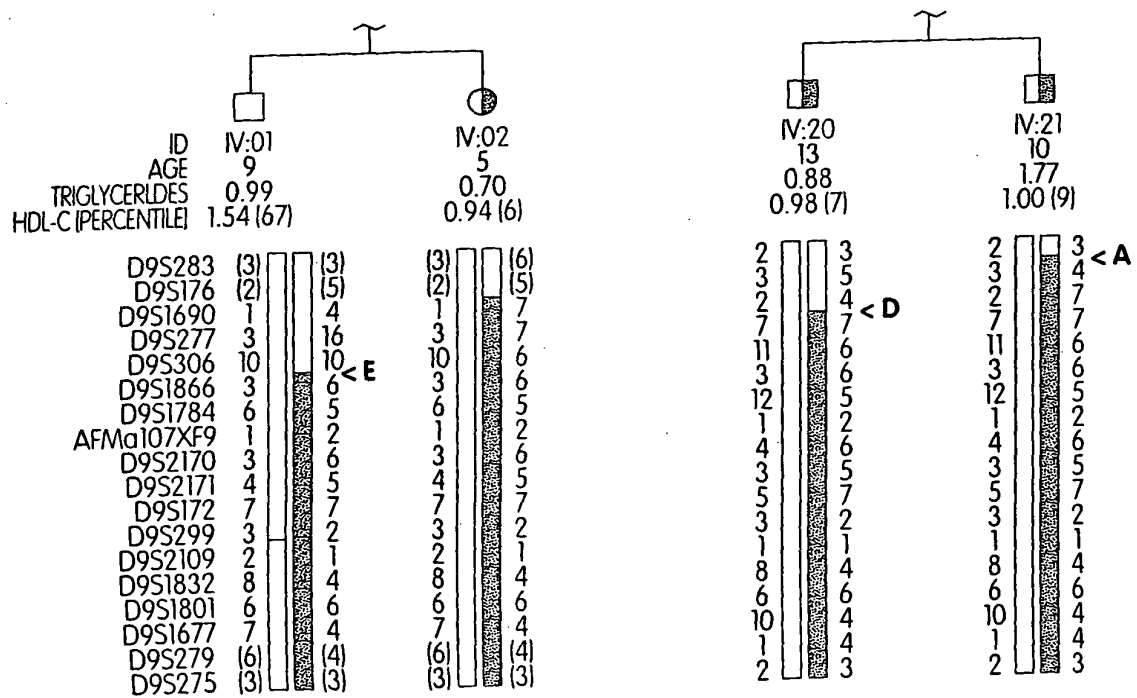
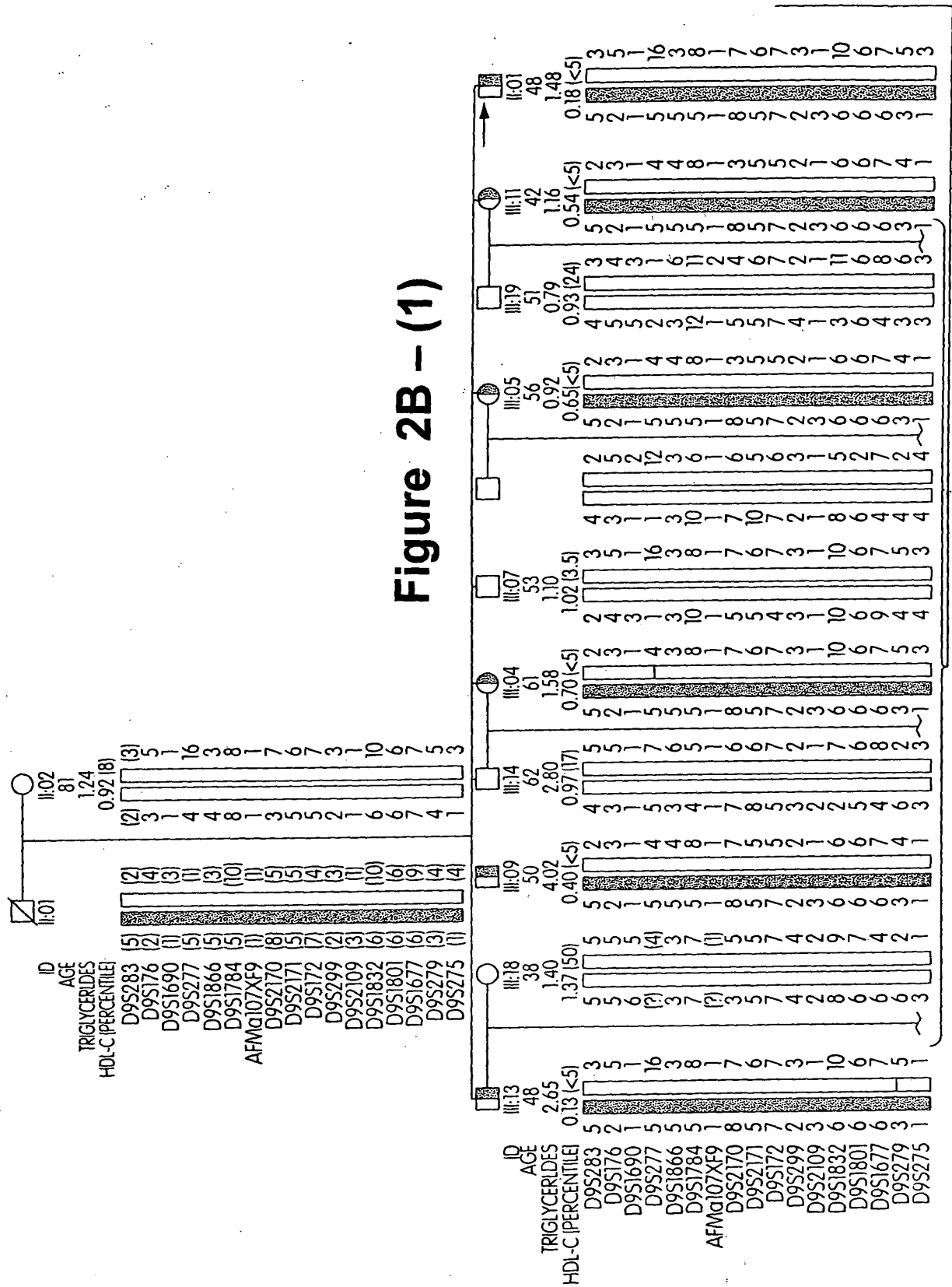


Figure 2A – (2)

Figure 2B - (1)



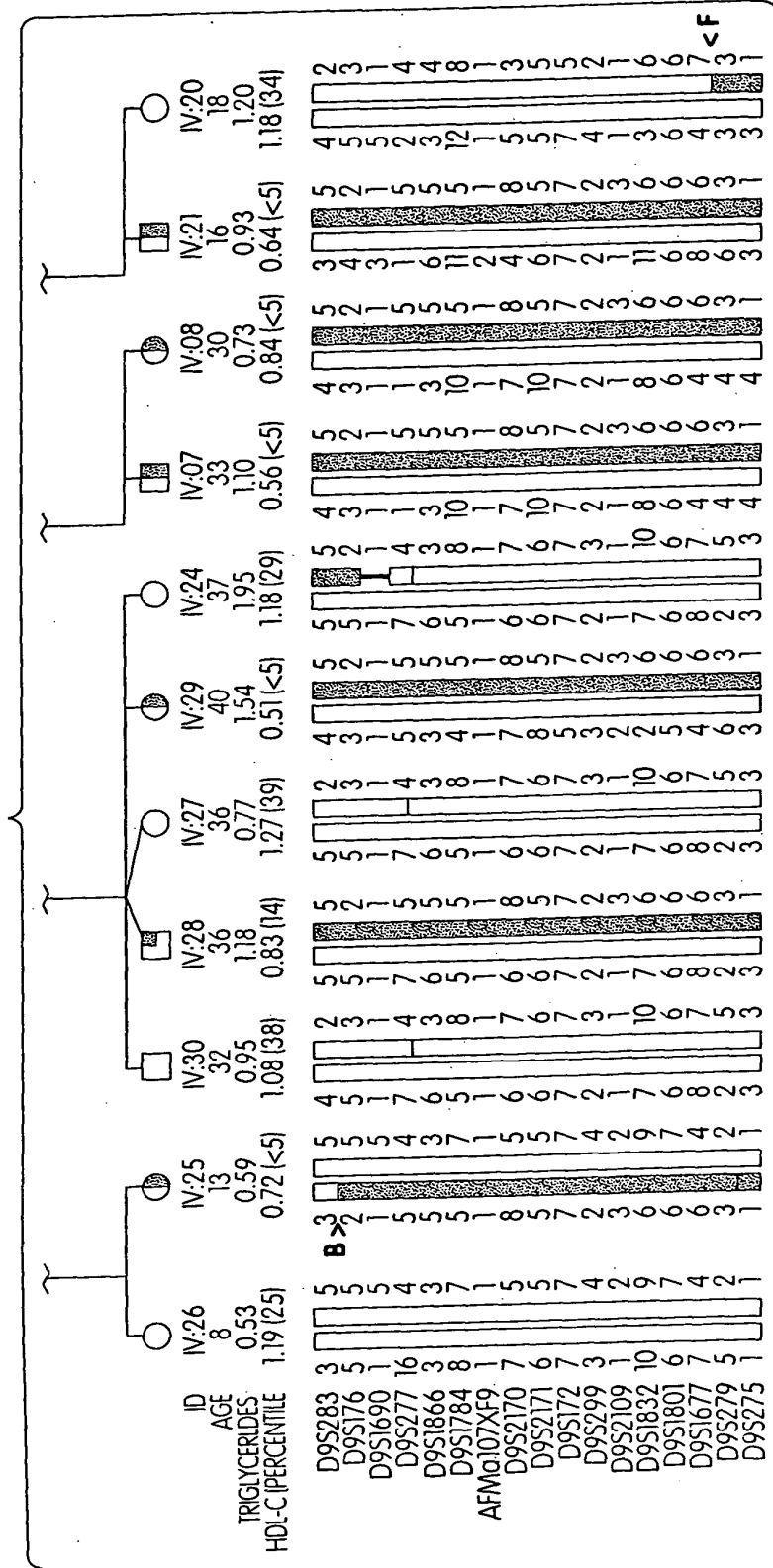


Figure 2B - (2)

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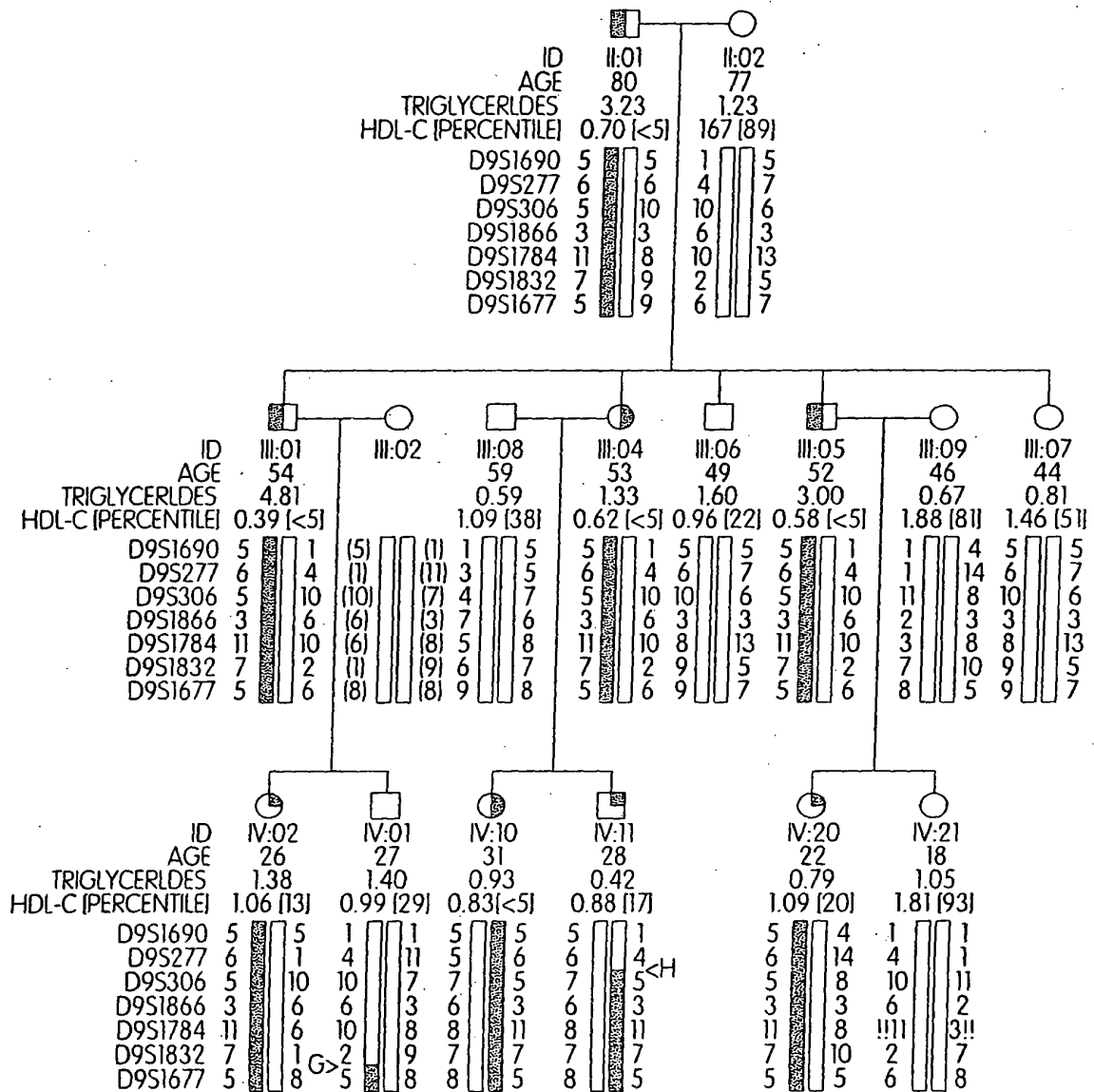


Fig. 2C

10/76

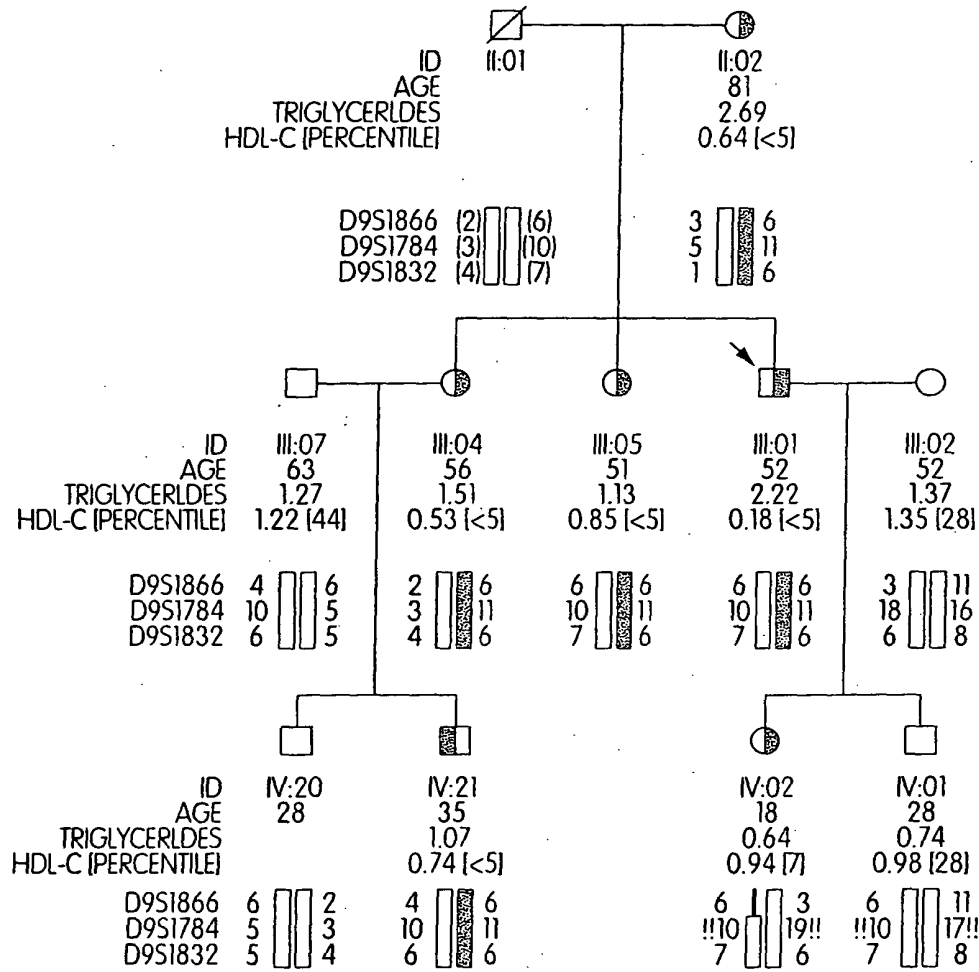
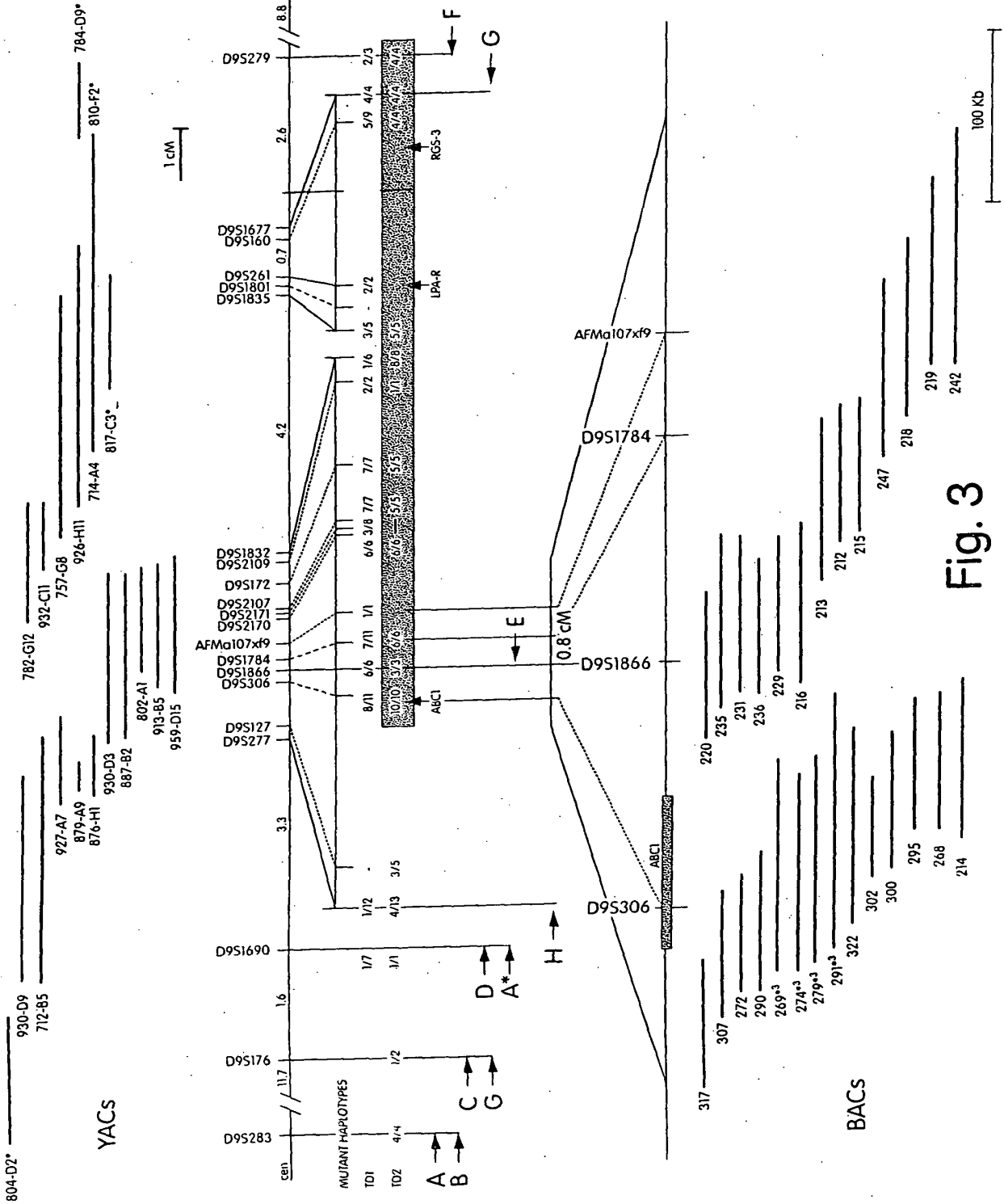


Fig. 2D



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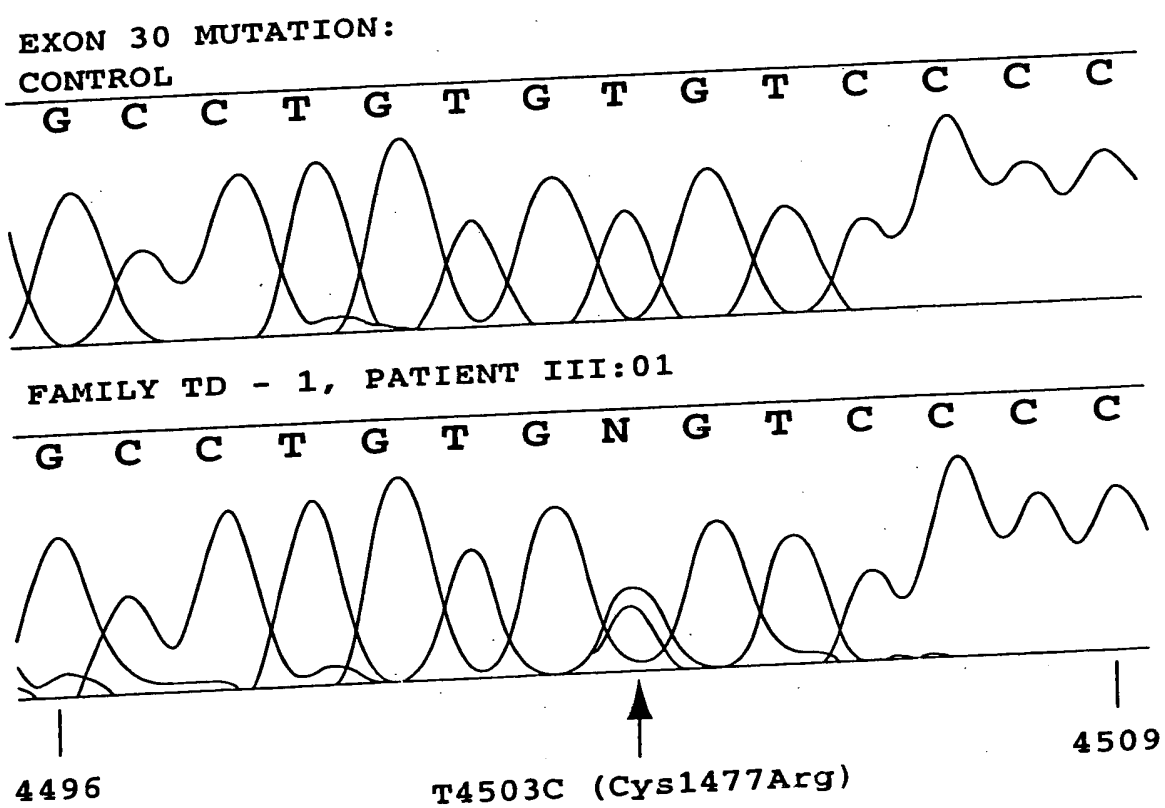


Fig. 4A

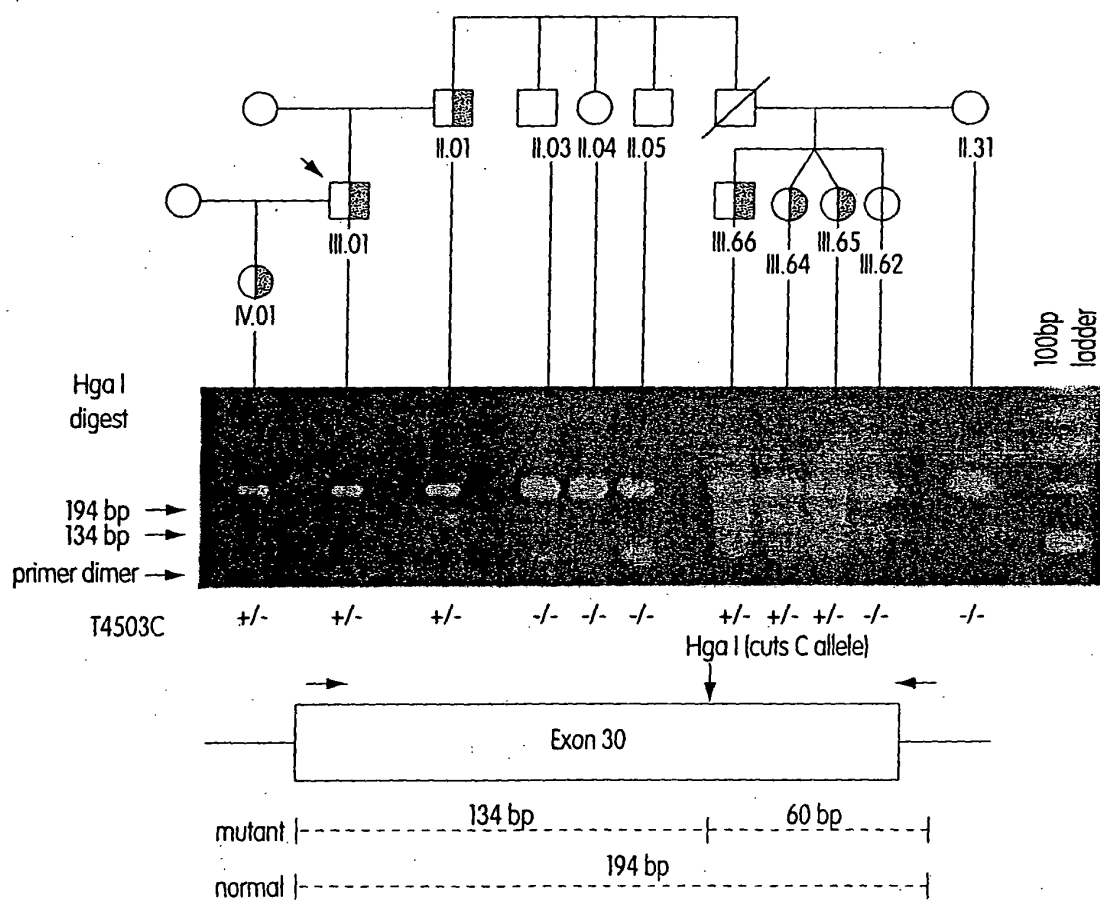


Fig. 4C

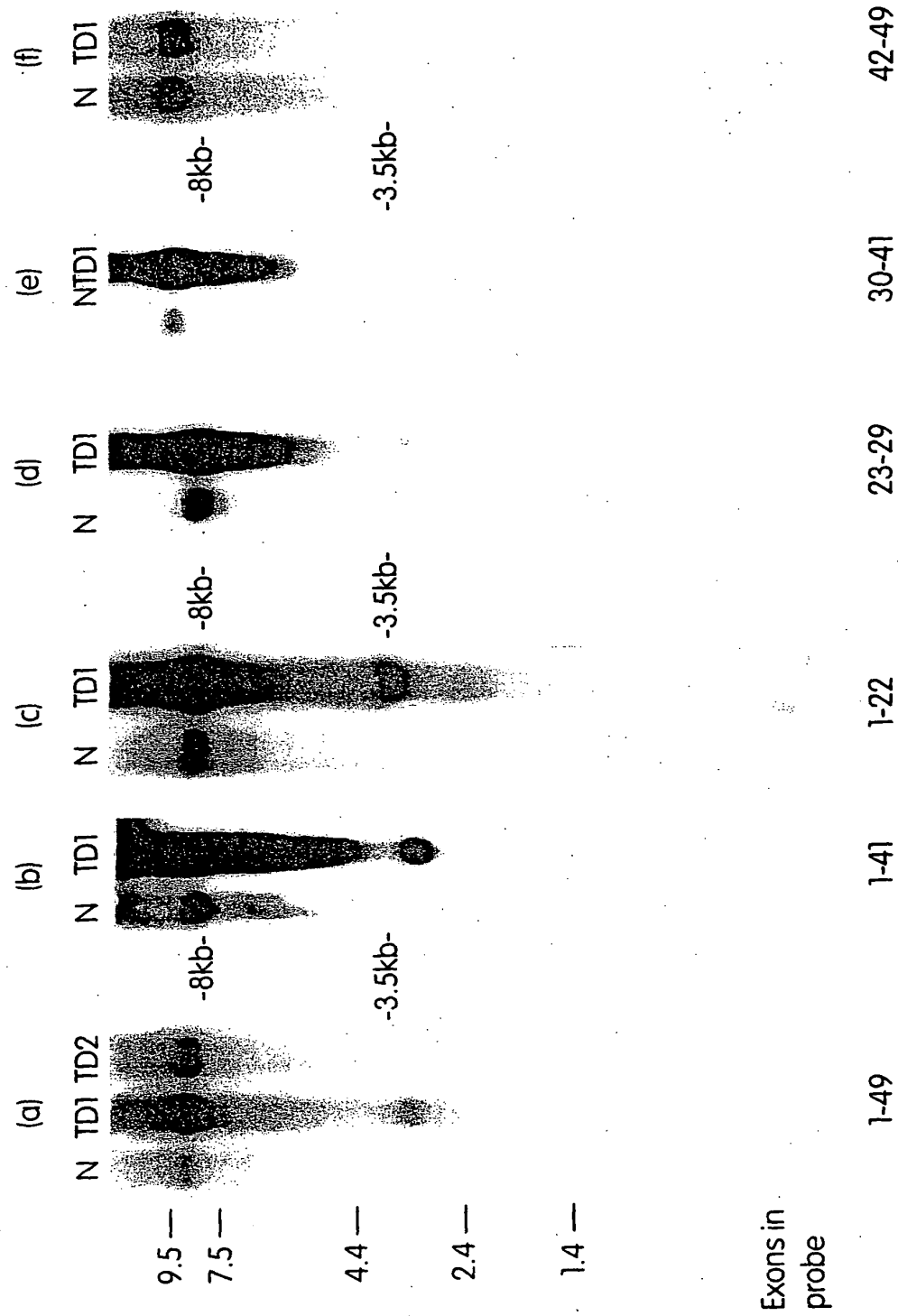
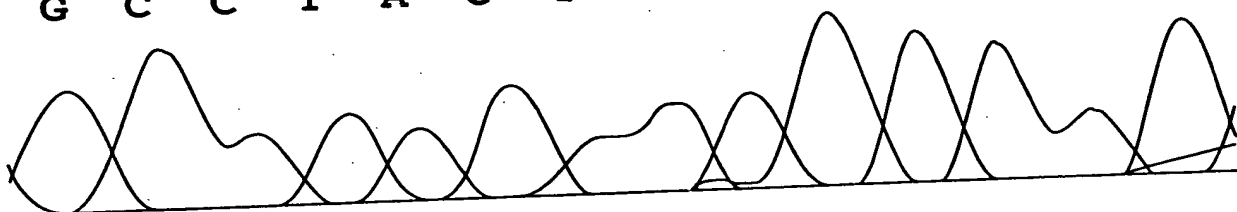


Fig. 4D

EXON 13 MUTATION:

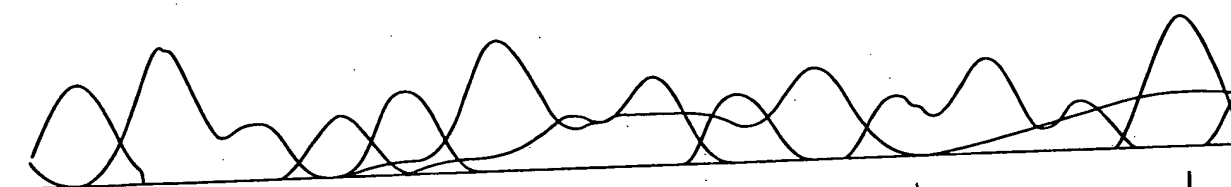
CONTROL

G C C T A C T T G C A G G A



FAMILY TD - 2, patient IV:10

G C C T A C T T G C G G G A



1854

A1864G (Q597R)

1876

Fig. 5A

EXON 13
TD-2

	1842		1864		1886					
wt sequence	tgggggggcttcgcctacttgcAggatgtggtggagcaggcaatc									
HUMAN_ABC1	N G G F A Y L Q D V V E Q A F									
MOUSE_ABC1	N G G F A Y L Q D V V E Q A F									
Patient	N G G F A Y L R D V V E Q A F									
CAEEL_ABC	- - - F M T V Q R A V D V A F									
Patient	tgggggggcttcgcctacttgcGggatgtggtggagcaggcaatc									

Fig. 5B

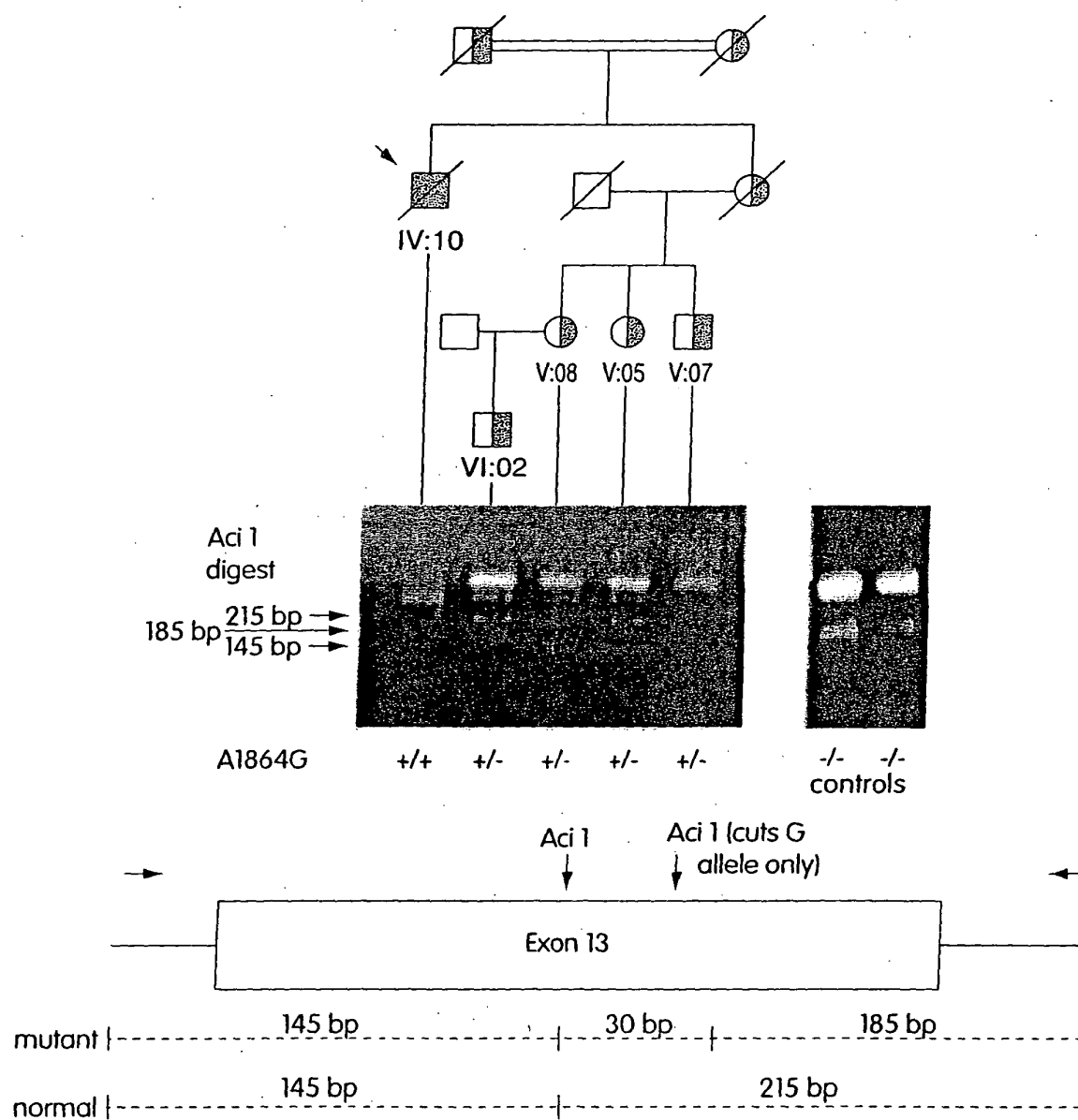


Fig. 5C

Exon 14: FHA - 1, patient III:01

T C A T T C C T C T T G T N N G C N C N G N N C N

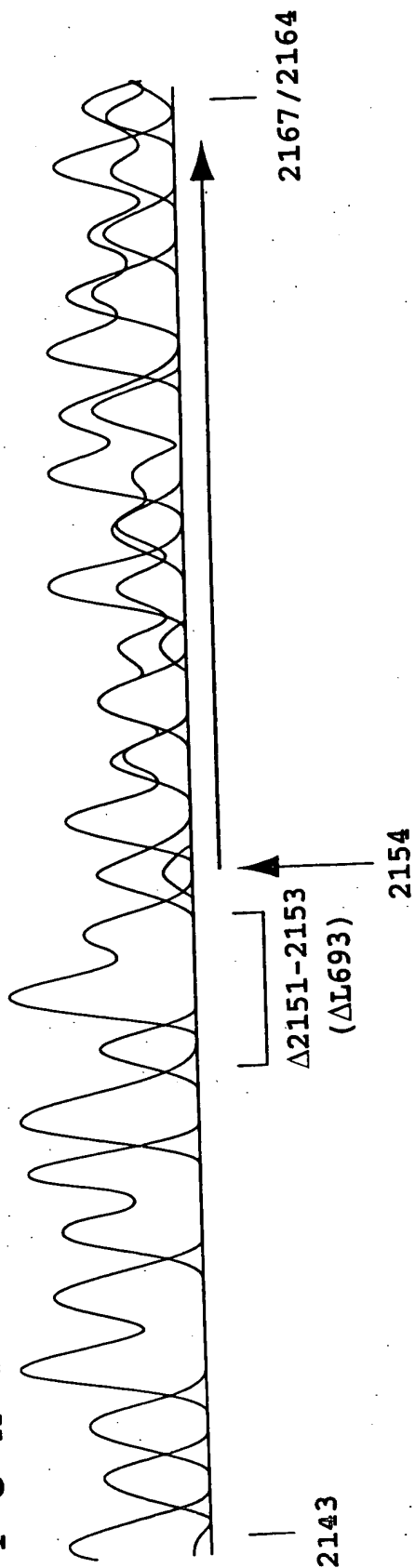


Fig. 6A

EXON 14
FHA-1

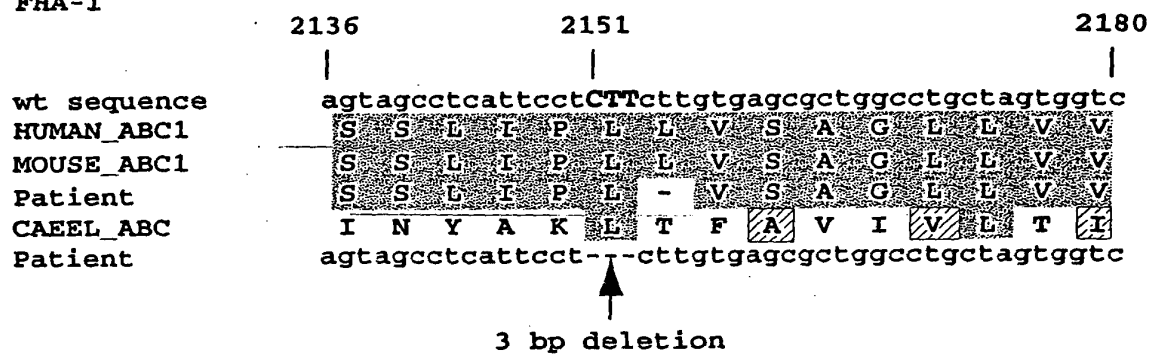


Fig. 6B



Fig. 6C

Exon 41: FHA - 3, patient III:01

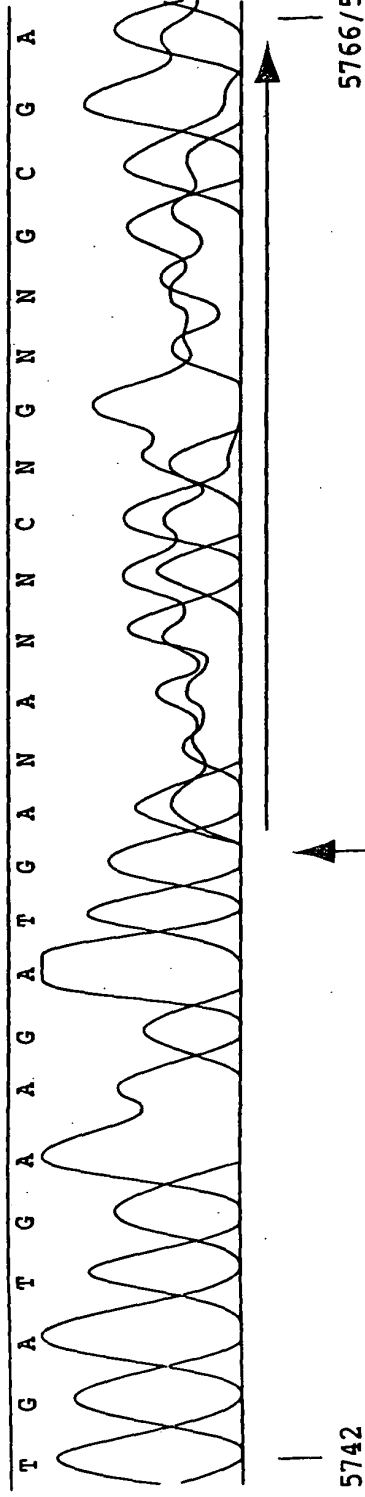


Fig. 6D

EXON 41
FHA-3

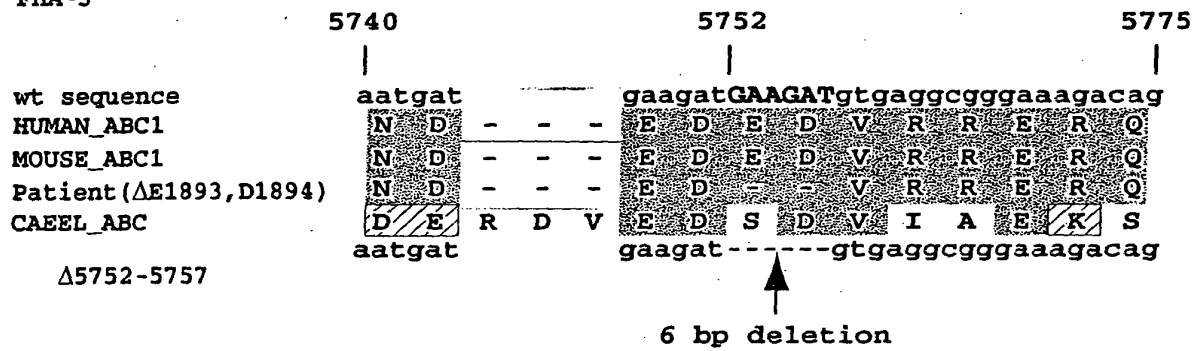
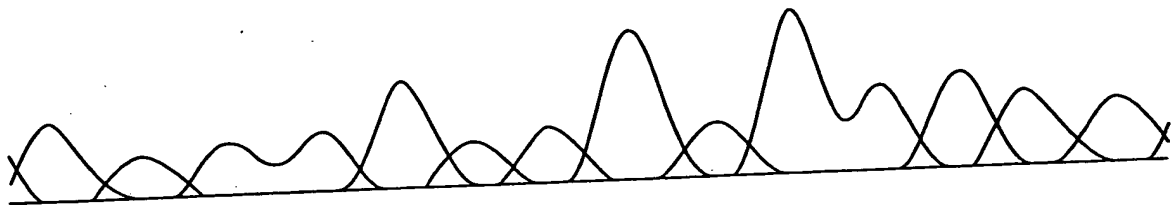


Fig. 6E

Exon 48 mutation:

Control

A G T T G T A C G A A T A G



Family FHA - 2, patient III:01

A G T T G T A N G A A T A G



6497 6510
C6504T (Arg2144STOP)

Fig. 6F

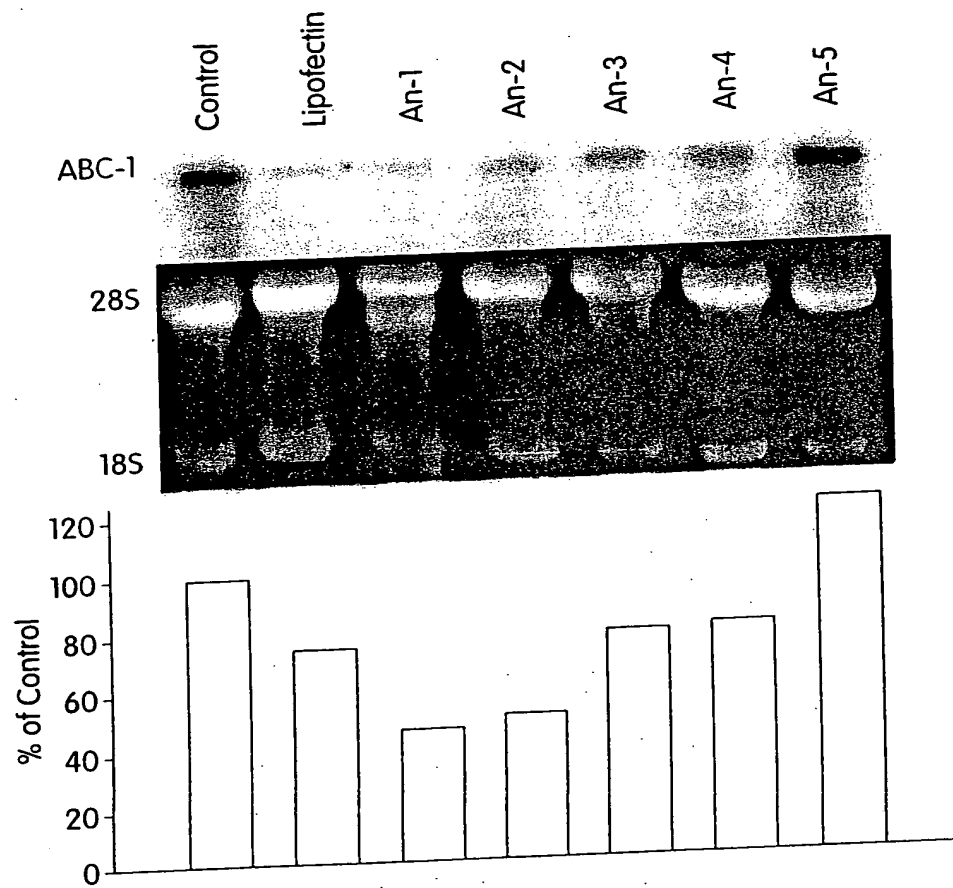


Fig. 7A

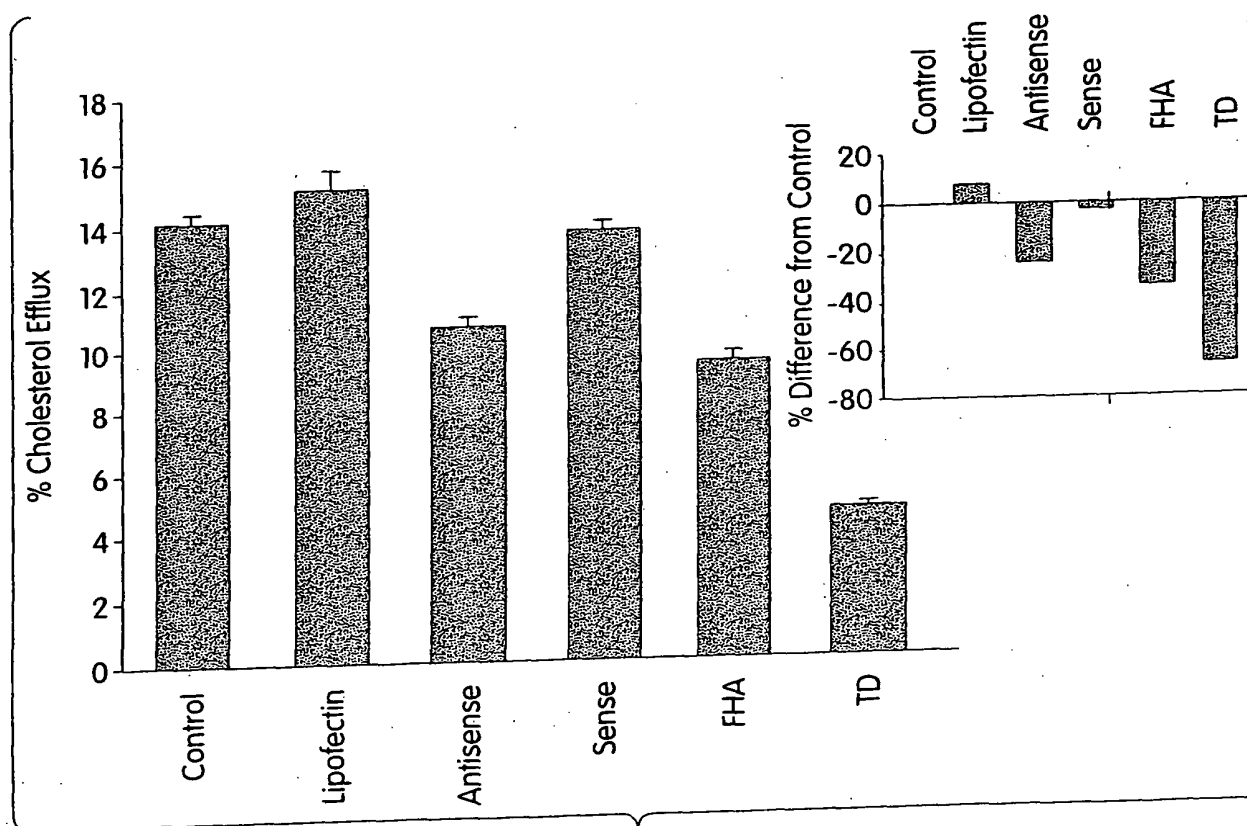


Fig. 7B

27176

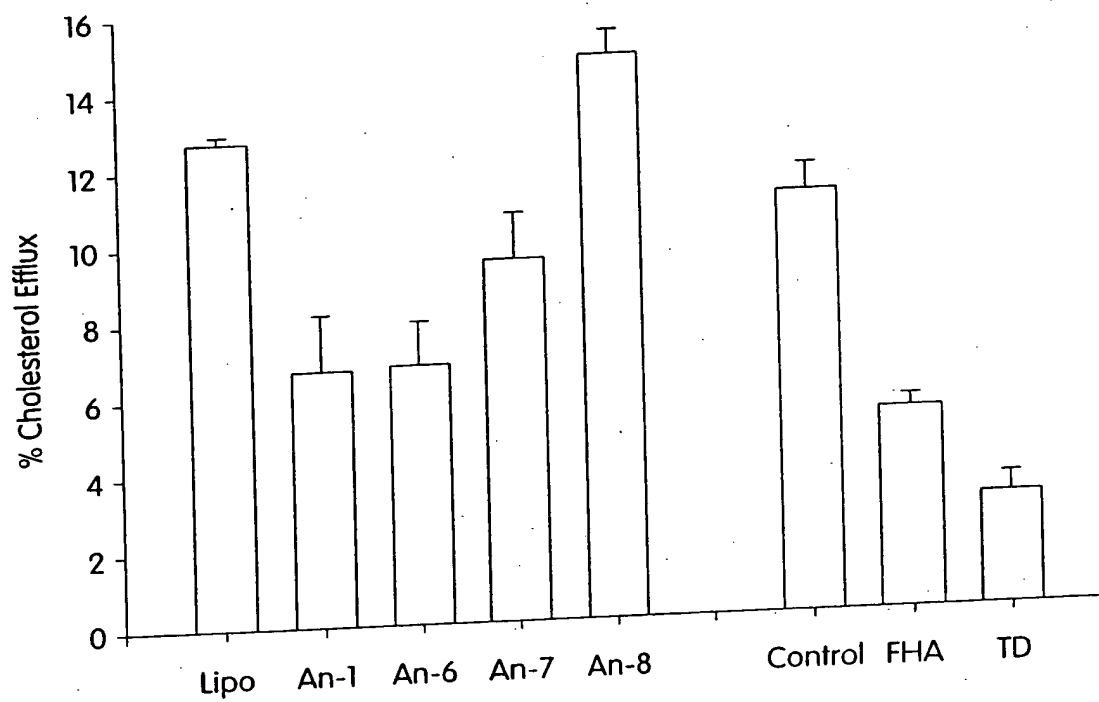


Fig. 7C

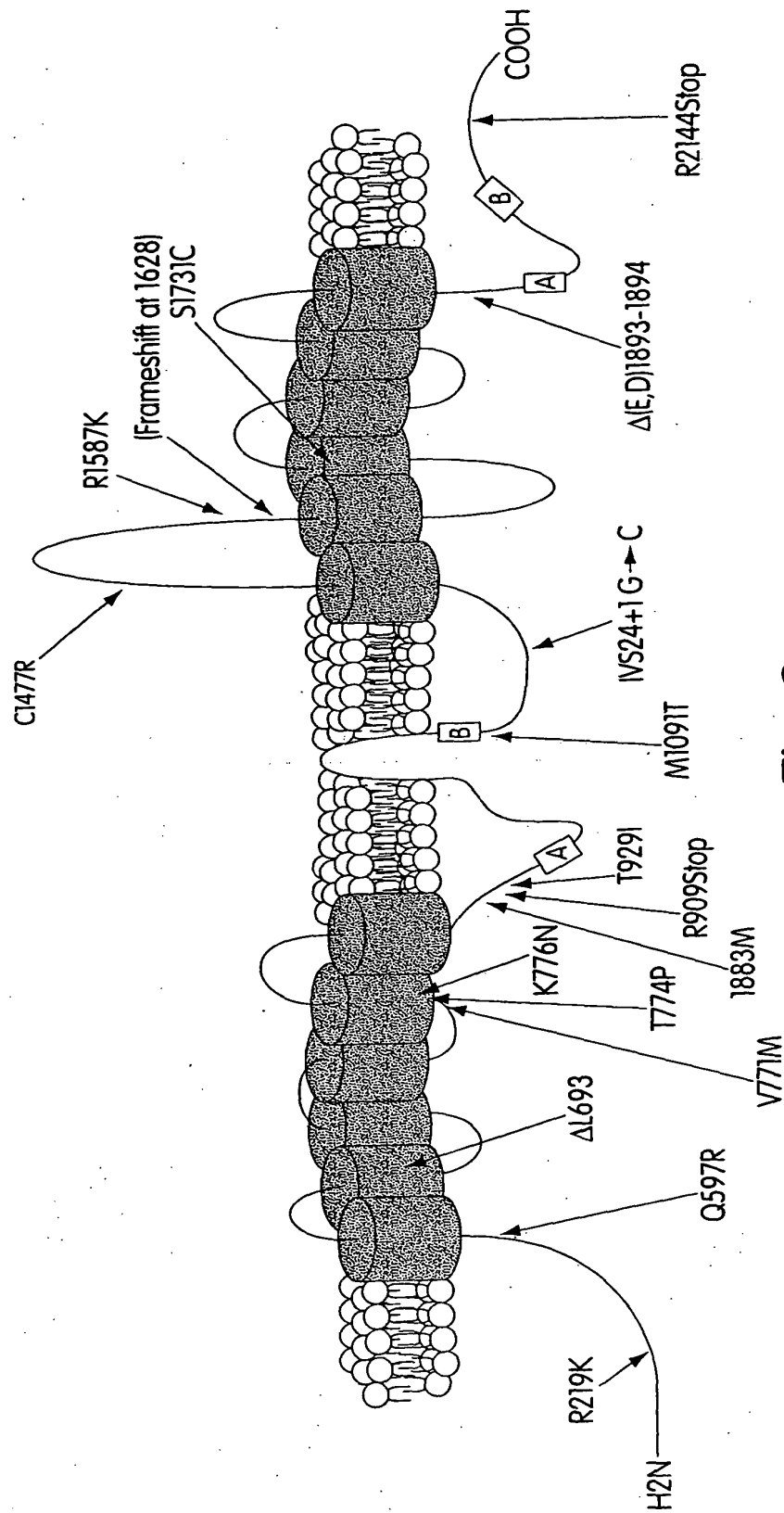


Fig. 8

SEQ ID NO: 1

MACWPQLRLLLWKNLTFRRRQTCQLLLEVAWPLFIFLILISVRLSYPPYEQHECHFPNKAMPSAGTLPWVQ
 GIICNANNPCFRYPTPGEAPGVGNFNKSIVARLFSADARRLLYSQKDTSMKDMRKVLRTLQQIKKSSSNL
 KLQDFLVDNETFSGFLYHNLSLPKSTVDKMLRADVILHKVFLQGYQLHLTSLCNGSKSEMIQLGDQEVSE
 LCGLPREKLAAAEVRLRSNMDILKPILRTLNSTSPFPKELAEATKLLHSLGTLAQELFSMRSWSDMRQE
 VMFLTNVNSSSSSTQIYQAVSRIVCGHPEGGLKIKSLNWYEDNNYKALFCGNGTEEDAETFYDNSTTPYC
 NDLMKNLESSPLSRIIWKALKPLLVGKILYTPDTPATRQVMAEVNKTFFQELAVFHDLEGWHEELSPKIWTF
 MENSQEMDLVRMLLDSRDNDHFWEQQLDGLDWTADQDIVAFLAKHPEDVQSSNGSVYTWREAFNETNQAIRT
 ISRFMECVNLNKLEPIATEVWLINKSMELDERKFWAGIVFTGITPGSIELPHVKYKIRMDIDNVERTNK
 IKDGYWDPGRADPFEDMRVWGGFAYLQDVVEQAIIRVLTGTEKKTGVYMQMPYPCYVDDIFLRVMSRS
 MPLFMTLAWIYSVAVIIGKIVYEKEARLKETMRIMGLDNSILWFSWFISSLIPLLVSAGLLVILKLGILL
 PYSDPVSVFVFLSVFAVVTILQCFLISTLFSRANLAAACGGIIYFTLYLPYVLCVAVQDYVGFTLKIIFASL
 LSPVAFGFGCEYFALFEEQIGVQWDLNLFESPVEEDGFNLTTSSVMMLFDTFLYGVMTWYIEAVFPGQYGI
 PRPWYFPCTKSYWFGGEESDEKSHPGSNQKRRISEICMEEEPHTLKLGVSIQNLVKVYRDGMKVAVDGLALNF
 YEGQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYILGKDIRSEMSTIRQNLGVCQPHNVLFDMLTVEEHI
 WFYARLKGLSEKHVKAEMEOMALDVGLPSSKLKSKTSQSLSCGMQRKLSVALAFVGGSKVVILDEPTAGVDP
 YSRRGIWELLKYRQGRITILSTHMDADVLGDRIAIISHGKLCVGSLSFLKNQLGTGYLTLVKKDVE
 SSLSSCRNSSSTVSYLKEDSVSQSSSDAGLGSDESHTLTIDVSAISNLIRKHVSEARLVEDIGHELTIV
 LPYEAKEGAFVELFHEIDRLSDLGISSYGISETTLEEIFLKVAEESGVDAETSDGTLPARNRRAFGDK
 QSLRPFTEDDAADPNDSIDPESRETDLLSGMDGKGSYQVKGWKLTOQQFVALLWKRLLIARRSRKGFFA
 QIVLPAVFVCIALVFSILVPPFGKYPSLELQPMWYNEQYTFVSNDAPEDTGTLELLNALTKDPGFGTRCME
 GNPIDTPCQAGEEWTAPVPQTIMDLFQNGNWTMNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRKQ
 NTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQEVNDAIKQMKKHL
 KLAkdSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVINNAILRANLQKGENPSHYGITAFN
 HPLNLTKQQLSEVALMTTSVDVLVSICVIFAMSFVPASFVFLIQERVSKAKHLQFISGVKPVIIYWLSNFV
 WDMCNYVVPATLVIIIFICFQKSYVSSTNLPVLALLLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNL
 FIGINGSVATFVLELFTDNKLNINDILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSW
 DLVGRNLFAMAVEGVVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGGGQNDILEIKEL
 TKIYRRKRKPAVDRICVGIPPGECFGLLGVNGAGKSSTFKMLTGDTTVTRGDAFLNKNSILSNIHEVHQNM
 GYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKVGWEAIRKLGLVKYGEKYAGNYSNGNRKLSTAMAL
 IGGPPVVFLEPPTGMDPKARRFLWNCALSVVKEGRSVVLTSHSMEECEALCTRMAIMVNGRFRCLGSVQH
 LKNRFGDGYTIVVRIAGSNPDLKPVDFFGLAFPGSVLKEKHRNMLQYQLPSSLSLARIFSILSQSKRL
 HIEDYSVSQTTLDQVFVNFAKDQSDDHLDLSDLSLKNQTVVDVAVLTSFLQDEKVKEYSV*

Fig. 9A

SEQ ID NO: 2

GTCCCTGCTGTGAGCTCTGGCCGCTGCCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTG
CTGGCTGAGGGAACATGGCTTGTGGCCTCAGCTGAGGTGCTGCTGTGGAAGAACCTCA
CTTTCAGAAGAAGACAAACATGTCAGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCT
TCCTGATCCTGATCTCTGTTCCGCTGAGCTACCCACCCTATGAACAACATGAATGCCATT
TTCCAAATAAAGCCATGCCCTCTGCAGGAACACTTCCTTGGGTTCAGGGGATTATCTGTA
ATGCCAACAAACCCCTGTTCCGTTACCCGACTCCTGGGGAGGCTCCCGGAGTTGTTGGAA
ACTTTAACAAATCCATTGTGGCTCGCCTGTTCTCAGATGCTCGGAGGCTTCTTTTATACA
GCCAGAAAGACACCAGCATGAAGGACATGCGCAAAGTTCTGAGAACATTACAGCAGATCA
AGAAATCCAGCTCAAACCTGAAGCTTCAAGATTTCTGGTGGACAATGAAACCTTCTCTG
GGTTCCTGTATCACAACCTCTCTCTCCCAAAGTCTACTGTGGACAAGATGCTGAGGGCTG
ATGTCATTCTCCACAAGGTATTTTGGCAAGGCTACCAGTTACATTTGACAAGTCTGTGCA
ATGGATCAAAATCAGAAGAGATGATTCAACTTGGTGACCAAGAAGTTTCTGAGCTTTGTG
GCCTACCAAGGGAGAAACTGGCTGCAGCAGAGCGAGTACTTCGTTCCAACATGGACATCC
TGAAGCCAATCCTGAGAACAATAACTCTACATCTCCCTTCCCGAGCAAGGAGCTGGCTG
AAGCCACAAAAACATTGCTGCATAGTCTTGGGACTCTGGCCCAGGAGCTGTTTCAGCATGA
GAAGCTGGAGTGACATGCGACAGGAGGTGATGTTTCTGACCAATGTGAACAGCTCCAGCT
CCTCCACCCAAATCTACCAGGCTGTGTCTCGTATTGTCTGCGGGCATCCCGAGGGAGGGG
GGCTGAAGATCAAGTCTCTCAACTGGTATGAGGACAACAATAACAAAGCCCTCTTTGGAG
GCAATGGCACTGAGGAAGATGCTGAAACCTTCTATGACAACCTCTACAACCTCTTACTGCA
ATGATTTGATGAAGAATTTGGAGTCTAGTCCCTCTTCCCGCATTATCTGGAAGCTCTGA
AGCCGCTGCTCGTTGGGAAGATCCTGTATACACCTGACACTCCAGCCACAAGGCAGGTCA
TGGCTGAGGTGAACAAGACCTTCCAGGAACCTGGCTGTGTTCCATGATCTGGAAGCCATGT
GGGAGGAACTCAGCCCCAAGATCTGGACCTTCATGGAGAACAGCCAAGAAATGGACCTTG
TCCGGATGCTGTTGGACAGCAGGGACAATGACCACTTTTGGGAACAGCAGTTGGATGGCT
TAGATTGGACAGCCCAAGACATCGTGGCGTTTTTGGCCAAGCACCCAGAGGATGTCCAGT
CCAGTAATGGTTCTGTGTACACCTGGAGAGAAGCTTTCAACGAGACTAACCAGGCAATCC
GGACCATATCTCGCTTCATGGAGTGTGTCAACCTGAACAAGCTAGAACCATAGCAACAG
AAGTCTGGCTCATCAACAAGTCCATGGAGCTGCTGGATGAGAGGAAGTTCTGGGCTGGTA
TTGTGTTCACTGGAATTACTCCAGGCAGCATTGAGCTGCCCCATCATGTCAAGTACAAGA
TCCGAATGGACATTGACAATGTGGAGAGGACAAATAAAATCAAGGATGGGTACTGGGACC
CTGGTCTCGAGCTGACCCCTTTGAGGACATGCGGTACGTCTGGGGGGGCTTCGCCTACT
TGCAGGATGTGGTGGAGCAGGCAATCATCAGCGTGCTGACGGGCACCCGAGAAGAAAACCTG

Fig. 9B

GTGTCATATGCAACAGATGCCCTATCCCTGTTACGTTGATGACATCTTCTGCCGGTGA
TGAGCCGGTCAATGCCCCCTTTCATGACGCTGGCCTGGATTTACTCAGTGGCTGTGATCA
TCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATCATGGGCC
TGGACAACAGCATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCTCTTCTGTGA
GCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCCA
GCGTGGTGTGTTGCTTCTCTGTCCGTGTTTGTCTGTGGTGACAACTCTGCAGTGCTTCTGA
TTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGCATCATCTACTTCA
CGCTGTACCTGCCCTACGTCTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCA
AGATCTTCGCTAGCCTGCTGTCTCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCC
TTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCTGTGGAGG
AAGATGGCTTCAATCTCACCCTTCGGTCTCCATGATGCTGTTTGACACCTTCTCTATG
GGGTGATGACCTGGTACATTGAGGCTGTCTTTCCAGGCCAGTACGGAATTTCCAGGCCCT
GGTATTTTCTTGCACCAAGTCTACTGGTTTGGCGAGGAAAGTGATGAGAAGAGCCACC
CTGGTTCCAACCAGAAGAGAATATCAGAAATCTGCATGGAGGAGGAACCCACCCACTTGA
AGCTGGGCGTGTCCATTGAGAACCTGGTAAAAGTCTACCGAGATCGGATGAAGGTGGCTG
TCGATGGCCTGGCACTGAATTTTATGAGGGCCAGATCACCTCTTCTGGGCCACAATG
GAGCGGGGAAGACGACCACCATGTCAATCCTGACCGGGTGTTCCTCCCCGACCTCGGGCA
CCGCTACATCCTGGGAAAAGACATTGCTCTGAGATGAGCACCATCCGGCAGAACCTGG
GGTCTGTCCCCAGCATAACGTGCTGTTTGACATGCTGACTGTGGAAGAACACATCTGGT
TCTATGCCCCGCTTGAAAGGCTCTCTGAGAAGCACGTGAAGGCGGAGATGGAGCAGATGG
CCCTGGATGTTGGTTTGCCATCAAGCAAGCTGAAAAGCAAAACAAGCCAGCTGTGAGGTG
GAATGCAGAGAAAGCTATCTGTGGCCTTGGCCTTTGTGCGGGGATCTAAGGTTGTATTCT
TGGATGAACCCACAGCTGGTGTGGACCTTACTCCCGCAGGGGAATATGGGAGCTGCTGC
TGAAATACCGACAAGGCCGACCATTTATCTCTCTACACACCACATGGATGAAGCGGACG
TCCTGGGGGACAGGATTGCCATCATCTCCCATGGGAAGCTGTGCTGTGTGGGCTCTCTCC
TGTTTCTGAAGAACCAGCTGGGAACAGGCTACTACCTGACCTTGGTCAAGAAAGATGTGG
AATCCTCCCTCAGTTCTCTGCAGAAACAGTAGTAGCACTGTGTACATACCTGAAAAAGGAGG
ACAGTGTCTCTCAGAGCAGTTCTGATGCTGGCCTGGGCAGCGACCATGAGAGTGACACGC
TGACCATCGATGTCTCTGCTATCTCAACCTCATCAGGAAGCATGTGTCTGAAGCCCGGC
TGGTGGAAAGACATAGGGCATGAGCTGACCTATGTGCTGCCATATGAAGCTGCTAAGGAGG
GAGCCTTTGTGGAACCTTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCATTCTTA
GTTATGGCATCTCAGAGACGACCTTGAAGAAATATTCCTCAAGGTGGCCGAAGAGAGTG
GGGTGGATGCTGAGACCTCAGATGGTACCTTGCCAGCAAGACGAAACAGGCGGCCCTTCG
GGGACAAGCAGAGCTGTCTTCGCCCGTTCACTGAAGATGATGCTGCTGATCCAAATGATT

Fig. 9C

CTGACATAGACCCAGAATCCAGAGAGACAGACTTGCTCAGTGGGATGGATGGCAAAGGGT
 CCTACCAGGTGAAAGGCTGGAACCTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAGA
 GACTGCTAATTGCCAGACGGAGTCGGAAAGGATTTTTTGTCTCAGATTGTCTTGCCAGCTG
 TGTTTGTCTGCATTGCCCTTGTGTTTTCAGCCTGATCGTGCCACCCCTTTGGCAAGTACCCCA
 GCCTGGAACCTTCAGCCCTGGATGTACAACGAACAGTACACATTTGTCAGCAATGATGCTC
 CTGAGGACACGGGAACCCCTGGAACCTCTTAAACGCCCTCACCAGAACCCCTGGCTTCGGGA
 CCCGCTGTATGGAAGGAAACCAATCCCAGACACGCCCTGCCAGGCAGGGGAGGAAGAGT
 GGACCACTGCCCCAGTTCCCCAGACCATCATGGACCTCTTCCAGAATGGGAACGGACAA
 TGCAGAACCCCTTACCCTGCATGCCAGTGTAGCAGCGACAAAATCAAGAAGATGCTGCCTG
 TGTGTCCCCCAGGGGCAGGGGGGCTGCCCTCTCCACAAAGAAAACAAAACACTGCAGATA
 TCCTTCAGGACCTGACAGGAAGAAACATTTCCGATTATCTGGTGAAGACGTATGTGCAGA
 TCATAGCCAAAAGCTTAAAGAACAAGATCTGGGTGAATGAGTTTAGGTATGGCGGCTTTT
 CCCTGGGTGTGAGTAATACTCAAGCACTTCTCCGAGTCAAGAAGTTAATGATGCCATCA
 AACAAATGAAGAAACACCTAAAGCTGGCCAAGGACAGTTCTGCAGATCGATTTCTCAACA
 GCTTGGGAAGATTTATGACAGGACTGGACACCAGAAATAATGTCAAGGTGTGGTTCAATA
 ACAAGGGCTGGCATGCAATCAGCTCTTTCTGAATGTCAATCAACAATGCCATTCTCCGGG
 CCAACCTGCAAAAGGGAGAGAACCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCC
 TGAATCTCACCAGCAGCAGCTCTCAGAGGTGGCTCTGATGACCACATCAGTGGATGTCC
 TTGTGTCCATCTGTGTCACTTTTGCAATGTCTTTCGTCCCAGCCAGCTTTGTGCTATTCC
 TGATCCAGGAGCGGCTCAGCAAAGCAAAACACCTGCAGTTTCATCAGTGGAGTGAAGCCTG
 TCATCTACTGGCTCTCTAATTTTGTCTGGGATATGTGCAATTACGTTGTCCCTGCCACAC
 TGGTCATTATCATCTTCATCTGCTTCCAGCAGAAGTCCATGTGTCTCCACCAATCTGC
 CTGTGCTAGCCCTTCTACTTTTGCTGTATGGGTGGTCAATCACACCTCTCATGTACCCAG
 CCTCCTTTGTGTTCAAGATCCCCAGCACAGCCTATGTGGTGCCTACCAGCGTGAACCTCT
 TCATTGGCATTAAATGGCAGCGTGGCCACCTTTGTGCTGGAGCTGTTACCGACAATAAGC
 TGAATAATATCAATGATATCCTGAAGTCCGTGTTCTTGATCTTCCACATTTTTTGCCTGG
 GACGAGGGCTCATCGACATGGTGAAAAACCAGCCAATGGCTGATGCCCTGGAAGGTTTG
 GGGAGAAATCGCTTTGTGTCAACATTATCTTGGGACTTGGTGGGACGAAACCTCTTCGCCA
 TGGCCGTGGAAGGGGTGGTGTCTTCTCATTACTGTTCTGATCCAGTACAGATTCTTCA
 TCAGGCCCAGACCTGTAAATGCAAAGCTATCTCCTCTGAATGATGAAGATGAAGATGTGA
 GCGGGGAAAGACAGAGAATTCTTGATGGTGGAGGCCAGAATGACATCTTAGAAATCAAGG
 AGTTGACGAAGATATATAGAAGGAAGCGGAAGCCTGCTGTTGACAGGATTTGCGTGGGCA
 TTCCTCCTGGTGAGTGCTTTGGGCTCCTGGGAGTTAATGGGGCTGGAAAATCATCAACTT
 TCAAGATGTTAACAGGAGATACCACTGTTACCAGAGGAGATGCTTTCCTTAACAAAAATA

Fig. 9D

GTATCTTATCAAACATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGATG
 CCATCACAGAGCTGTTGACTGGGAGAGAACACGTGGAGTTCTTTGCCCTTTTGAGAGGAG
 TCCCAGAGAAAGAAGTTGGCAAGGTTGGTGAGTGGGCGATTTCGAAACTGGGCCCTCGTGA
 AGTATGGAGAAAAATATGCTGGTAACATAGTGGAGGCAACAAACGCAAGCTCTCTACAG
 CCATGGCTTTGATCGGCGGGCTCCTGTGGTGTTCCTGGATGAACCCACCACAGGCATGG
 ATCCCAAAGCCCGGCGGTTCTTGTGGAATTGTGCCCTAAGTGTGTCAAGGAGGGGAGAT
 CAGTAGTGCTTACATCTCATAGTATGGAAGAATGTGAACCTCTTTGCAC'TAGGATGGCAA
 TCATGGTCAATGGAAGGTTCAAGGTGCCTTGGCAGTGTCCAGCATCTAAAAATAGGTTTG
 GAGATGGTTATACAATAGTTGTACGAATAGCAGGGTCCAACCCGGACCTGAAGCCTGTCC
 AGGATTTCTTTGGACTTGCATTTCTTGAAGTGTCTAAAAGAGAAACACCGGAACATGC
 TACAATACCAGCTTCCATCTTCATTATCTTCTCTGCCAGGATATTTCAGCATCCTCTCCC
 AGAGCAAAAAGCGACTCCACATAGAAGACTACTCTGTTTCTCAGACAACACTTGACCAAG
 TATTTGTGAAC'TTTGCCAAGGACCAAAGTGATGATGACCACTTAAAAGACCTCTCATTAC
 ACAAAAACCAGACAGTAGTGGACGTTGCAGTTCACATCTTTTCTACAGGATGAGAAAG
 TGAAAGAAAGCTATGTATGAAGAATCCTGTTTCATACGGGGTGGCTGAAAGTAAAGAGGAA
 CTAGACTTTCCTTTGCACCATGTGAAGTGTGTGGAGAAAAGACCCAGAAGTTGATGTGG
 GAAGAAGTAAACTGGATACTGTACTGATACTATTCAATGCAATGCAATTCAATGCAATGA
 AAACAAAATTCCATTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAG
 TGAAAGACTTGAATTTAGTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAA
 TGGACATATGGGTTTGAAC'TCACACTTTTTTTTTTTTTTTTTTTGTTCTGTGTATTCTCATT
 GGGGTTGCAACAATAATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAA
 GGTAATGCACATCCTCATTCAC'TAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGA
 CACATCCATTGCTGGCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTT
 TGAAGCACCATGGTGTGTCTATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCA
 ACATTGAATATCAGTTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCC
 TCTGATAAGCTGTTCTGGTGGCAGTAACATGCAACAAAAATGTGGGTGTCTCCAGGCACG
 GGAAACTTGGTTCCATTGTTATATTGTCTATGCTTCGAGCCATGGGTCTACAGGGTCAT
 CCTTATGAGACTCTTAAATATACTTAGATCCTGGTAAGAGGCAAAGAATCAACAGCCAAA
 CTGCTGGGGCTGCAACTGCTGAAGCCAGGCCATGGGATTAAAGAGATTGTGCGTTCAAAC
 CTAGGGAAGCCTGTGCCCATTGTCTCTGACTGTCTGCTAACATGGTACACTGCATCTCAA
 GATGTTTATCTGACACAAGTGTATTATTTCTGGCTTTTTGAATTAATCTAGAAAATGAAA

Fig. 9E

Exon Forward Primer (bp)	SEQ ID No.	Reverse Primer	SEQ ID No.	intron(kb)	intron (kb)
exon 1 140 GGCTGGATTAGCAGTCTCA	70	ATCCCCAACTCAAAACCACA	119	intron 1	>6.413
exon 2 94 GGATTCCAGATCCAGTG	71	AAGTCCAAATTTAGCCACGTT	120	intron 2	>4.241
exon 3 142 GACAGACTTGGCATGAAGCA	72	CCAGCCATTCAAATTTCTCC	121	intron 3	>1.248(1.6)
exon 4 119 GCACCTGGCAGTCACTTCNG	73	GGGTGCAGTCAATTTCCAAT	122	intron 4	>1.512
exon 5 122 CGTTCTCCACTGTCCCAT	74	CCCTTCCACCACTTACAA	123	intron 5	>1.796(3)
exon 6 177 ACTTCAAGGACCCAGCTTCC	75	TGTCCAAGGAAAGCCTCAC	124	intron 6	>2.726 (10)
exon 7 93 TCGGTTCTTGTGTTAACTCA	76	AGGACCTCTGCCAGACTCA	125	intron 7	4.975
exon 8 241 TCCCAAGGCTTGGAGATGAC	77	AGGAGATGACACAGGCCAAG	126	intron 8	>2.311(.5)
exon 9 140 GGCTCCAAAGCCCTGTAA	78	CGCACACCTCTGAAGCTACC	127	intron 9	0.332
exon 10 117 GCTGCTGTGATGGGTATCT	79	ACCTCACTCACACCTGGGA	128	intron 10	4.208
exon 11 198 TTTGTAATTTTGTAGTCTCTCA	80	GCCTCTGCTGAACCTTAT	129	intron 11	0.747
exon 12 206 TAGTCAGCCCTTGCCTCTA	81	CAAAATCATGACACCAAGTTGAG	130	intron 12	0.523
exon 13 177 AAAGGGCTTGGTAAGGGTA	82	CATGCACATGCACACACATA	131	intron 13	1.787
exon 14 223 GATGTGGTCTCCCTCTAGC	83	CCTTAGCCCGTGTGAGCTA	132	intron 14	1.747
exon 15 222 CAAGTGAGTCTTGGGATG	84	TGCTTTTATTTCAGGGACTCCA	133	intron 15	1.059
exon 16 205 GCAATTCAAATTTCTCCAGG	85	CCCATGCACTGCAGAGATTC	134	intron 16	1.105
exon 17 114 TCAAGGAGGAATGGACCTG	86	AAGCAGGAGACATCGCTT	135	intron 17	1.789
exon 18 172 CTGAAGTTCAAGCCAGTG	87	GGGATCAGCATGGTTTCTTA	136	intron 18	0.99
exon 19 132 TGCAGACTGAATGGAGATC	88	GCTTAAGTCCCACTCTCTCC	137	intron 19	1.307
exon 20 143 GCCAGGGGACACTGTATCT	89	ATTTTCTCTCCGATGTGTGT	138	intron 20	0.204
exon 21 138 AGGTCTCTGCTTCACTCA	90	TCACAGAAGCCTAGCCATGA	139	intron 21	0.706
exon 22 221 CCAGTGCTTACCCCTGCTAA	91	AACAGAGCAGGGAGATGGTG	140	intron 22	>0.866(1.7)
exon 23 73 CACACAACAGAGCTTCTTGA	92	TCTGCACCTCTCTCTCTCTG	141	intron 23	0.986
exon 24 203 ACCTGGAACAGGTGTGTGT	93	ACTGGGCCAACATTAATCA	142	intron 24	1.668
exon 25 49 GGGCTAACATGCCACTCAGTA	94	CTTCCCATCTCTGCACAAAC	143	intron 25	0.196

Figure 10A

exon 26	114	GTTGTTGCAGATGGGGAAG	144	GCTAAGGGCCATCCAAAGAA	intron 26	1.396	1.4
exon 27	149	CACCAGAAGAGGAGCATGG	145	TCAAGTGCATCTGGGCATAA	intron 27	1.649	1.6
exon 28	125	CTGGACTCGTAGGATTTGC	146	TCTGAAGTCCATTCCCTTGG	intron 28	>0.728(1.4)	1.4
exon 29	99	GCCTGTACAGAGAAATGCTT	147	CAATGTGGCATGCAAGTTGAT	intron 29	>2.589(3)	3
exon 30	190	TTACGGAATGATCCTGTGCTC	148	GAAGCTACCAGCCCATCCT	intron 30	1.521	1.5
exon 31	95	AGTCAGGTTTCCGGTCACAC	149	CATTTCCCCACACTGTTTCAG	intron 31	>0.944(\)	>0.9
exon 32	33	CCGTTCCCTTATATCCTCAGGTG	150	CCAAGGCTTCTTCAATCCA	intron 32	>1.062(/6.5)	>1.0
exon 33	106	CCTTGTACACACTCCGACTGA	151	GATCCGTTTAACTTCCCAAC	intron 33	1.475	1.5
exon 34	75	TGTTGTCCACAGTTCCAGA	152	ATGCCCTGCCAACTTTAC	intron 34	0.522	0.5
exon 35	170	TGAGGTTTATGGGCATGGTT	153	CTCTGCAGTGTTCCTCCCTAC	intron 35	1.228	1.2
exon 36	178	ATGTTTTCTCTGGCTGTGC	154	TATCAATCCATGGCCCTGAC	intron 36	>1.898(2)	2
exon 37	116	ATCTGCCCTTTCTTGTCTGA	155	AGAGTCCCTGCCCTCCTTCT	intron 37	0.112	0.1
exon 38	145	AGGGAGCTGCACAGTGGATA	156	AAGGCAGTCAGCAGTGTCAA	intron 38	1.545	1.5
exon 39	124	TCACTCCCATATTTCAAGACTTGA	157	GGGGAACATCCTGTGCTTAG	intron 39	1.087	1.1
exon 40	130	TGTTTATTGGAAGATCGGTGAA	158	CCATTGGTGAGTGTTCCTT	intron 40	0.265	0.3
exon 41	121	CGTTAGAGACTGAATCTTTGTCTTG	159	AGTCAGCAACTGCTGGGTT	intron 41	>0.622(0.9)	0.9
exon 42	63	AGTCTGCCCTTCCACAGTTG	160	ATGCTCCATCCTGGGCATAA	intron 42	0.909	0.9
exon 43	107	GGTAGTTACGTGTTAGGGCA	161	TCATGGATGATTTTATGTGCTTC	intron 43	2.355	2.4
exon 44	142	CAGGAACATTAGGCCAGATTG	162	GCCTGTGGAAGCCATAAG	intron 44	0.372	0.4
exon 45	135	CATGTATGTGTAGGACAGCATGA	163	GCCAATCATACAACAGCCCT	intron 45	>1.059(1.3)	1.3
exon 46	104	CTGTTTCAAAGATGCTTCTGC	164	TGATCGCATATTTCTACTTGGAAA	intron 46	0.483	0.5
exon 47	93	CCTAGGAAGCTTGAATGCTG	165	TCCCTTATTTTAGAGGCACCA	intron 47	0.659	0.7
exon 48	244	GGGTTCCAGGTTCAAGTAT	166	GATCAGGAATTCAGCACCAA	intron 48	0.941	0.9
exon 49	295	CTTGACCTAATTTCAACATCTGG	167	TGGGTTCCATATATAGATTTCA		>1.075	

Figure 10B

ERRORS IN PUBLIC SEQUENCE (differences between samples and Genbank entry AJ012376.1):				
Exon/Intron	Nucleotides	Amino Acid Change	Sequence difference/context	SEQ ID NO:
2	T150C A152G	no change	Public sequence: TGTACAGCTGTACTGGAGTGG Correct sequence: TGTACAGCTGTCTGGAAGTGG	168 169
7	C839T	no change	Public sequence: AGGAGCTGGCCGAAGCCACAA Correct sequence: AGGAGCTGGCTGAAGCCACAA	170 171
33	C4738T	T1495I	Public sequence: AATGATGCCACCAACAATG Correct sequence: AATGATGCCATCAACAATG	172 173
35	C5017T	P1588L	Public sequence: GAGGTGGCTCCGATGACCACA Correct sequence: GAGGTGGCTCTGATGACCACA	174 175
43	G5995A	R1914K	Public sequence: TTCCTTAAACAGAAATAGTATC Correct sequence: TTCCTTAAACAAAATAGTATC	176 177
48	C6577T	P2108L	Public sequence: GGAAGTGTTCAAAAGAGAAA Correct sequence: GGAAGTGTTCATAAAGAGAAA	178 179
49	G6899A	not applicable	Public sequence: AGTAAAGAGGGAGTAGACTTT Correct sequence: AGTAAAGAGGAACTAGACTTT	180 181
Mutations:				SEQ ID NO:
13	A1864G	Q597R	More common: GCCACTTTCAGGATGTGGTG Less common: GCCACTTTCGGGATGTGGTG	182 183
14	delta CTT 2151-3	delta L093	More common: CCTCATTCCTCTTCTGTGAGCG Less common: CCTCATTCCT/CTTGTGAGCG	184 185
15	G2385A	V771M	More common: GCAGGACTACGTGGGCTTCAC Less common: GCAGGACTACATGGGCTTCAC	186 187
18	C2799T	R909Stop	More common: AAAAGTCTACCGAGATGGGAT Less common: AAAAGTCTACTCAGATGGGAT	188 189
18	C2860T	T929I	More common: GGCCAGATCACCCTCTTCTGTG Less common: GGCCAGATCATCTCTCTTCTGTG	190 191
22	T3346C	M1091T	More common: ACACACCAATGGATGAAGCG Less common: ACACACCAACGGATGAAGCG	192 193

Figure 11A

Intron	(+1) G to C splice donor site	Altered transcript length	More common: Less common:	CCTGGAAGAACTAAGTTAAGT CCTGGAAGAACTAAGTTAAGT	194 195
30	T4503C	C1477R	More common: Less common:	GCTGCCGCTGTGTCCTCCCGG GCTGCCGCTGTGTCCTCCCGG	196 197
35	GG 4958-57 to C	frameshift at aa 1628	More common: Less common:	TAGCCATTTATGGAATTACTGCT TAGCCATTTATCAATTACTGCT	198 199
41	delta AAGATG 5752-7	delta (E.D)1893-1894	More common: Less common:	GATGAAGTGAAGATGTGAGCGGGA GATGAAGATG/TGAGCGGGA	200 201
48	G6504T	R2144Stop	More common: Less common:	AATAGTTGTACGAATAGCAGG AATAGTTGTATGAATAGCAGG	202 203
Promoter Variants:	Position Relative to Xenon cDNA	Position Relative to SEQ ID NO: 14 Containing Exon 1			SEQ ID NO:
1	G57C	8216	More common: Less common:	ACACGCTGGGGTCTCTGGCTG ACACGCTGGGGTCTCTGGCTG	204 205
5	(-14 ins. G	8158	More common: Less common:	GACCAACACGGCGTCCCTG GACCAACACGGCGTCCCTG	206 207
5	A (-1380 G	7780	More common: Less common:	CATTTTCTTAGAAAAGACAGCT CATTTTCTTAGAAGACAGCT	208 209
5	A (-1479 C	7681	More common: Less common:	GAAAATTAGTATCTAAGGAAG GAAAATTAGTCTGTAAGGAAG	210 211
5	A (-1738 G	7422	More common: Less common:	CTCCCGCTCCAGGTTACGCAAT CTCCCGCTCCCGGTTACGCAAT	212 213
5	A (-1045 G	7115	More common: Less common:	TATGTGCTGACCATGCGAGCTTGT TATGTGCTGACCGTGGAGCTTGT	214 215
5	A (-1113 G	7047	More common: Less common:	GTGACACCCACCGAGTAGGG GTGACACCCAGCGGAGTAGGG	216 217
5	(-1181 ins. CCTT	6979	More common: Less common:	AGTATCCCT/TGTTCCAGAGAA AGTATCCCTCCTTGTTCCAGAGAA	218 219

Figure 11B

Polymorphisms:					SEQ ID NO:
Exon/Intron	Nucleotides	Amino Acid Change		Sequence difference/context	
5	G548A	no change	More common: Less common:	CTGGTTCTCTGTATCACACC CTGGTTCTCTATATCACACC	220 221
6	G730A	R219K	More common: Less common:	GCCCTACCAAGGAGAACTG GCCCTACCAAGGAGAACTG	222 223
Intron 7	G(+)/2383 T	Not applicable	Allele 1: Allele 2:	TTAAAGGGGGTGTATTAGGA TTAAAGGGGGTGTATTAGGA	224 225
Intron 7	G(+)/3035 T	Not applicable	Allele 1: Allele 2:	GAAGAAATTTGTTTTTTGATT GAAGAAATTTTTTGTGATT	226 227
8	C1010T	no change	More common: Less common:	GCGGGCATCCCGAGGAGGGG GCGGGCATCTCGAGGAGGGG	228 229
8	G1022A	no change	More common: Less common:	AGGAGGGGGGCTGAAGATCA AGGAGGGGGGCTGAAGATCA	230 231
Intron 9	(-)/42 ins. G	Not applicable	More common: Less common:	AGGAGCCAAACGCTCATTTGT AGGAGCCAAAGCGCTCATTTGT	232 233
Intron 13	T(+)/24 A	Not applicable	More common: Less common:	AAGCCACTGTTTTTAAACAGT AAGCCACTGTATTAAACAGT	234 235
15	A2394C	T774P	More common: Less common:	CGTGGGCTTCACACTCAAGAT CGTGGGCTTCCCACTCAAGAT	236 237
15	G2402C	K776N	More common: Less common:	TCACACTCAAGATCTTCGCTG TCACACTCAACATCTTCGCTG	238 239
Intron 14	C(+)/16 T	Not applicable	Allele 1: Allele 2:	GCAGCCTCACCCGCTCTTCCC GCAGCCTCACTCGCTCTTCCC	240 241
17	A2723G	I883M	Allele 1: Allele 2:	AGAAGAGATATACAGAAATCT AGAAGAGATATCAGAAATCT	242 243
Intron 17	C(+)/2000 G	Not applicable	Allele 1: Allele 2:	GCCAGTGCCTGTGTCCTTA GCCAGTGCCTGTGTCCTTA	244 245

Figure 11C

21	T3233G	no change	More common: Less common:	GATCTAAGGTTGTCATCTGG GATCTAAGGTTGTCATCTGG	246 247
Intron 21	G(+1)118 T	Not applicable	Allele 1: Allele 2:	CTCTCTGTGAGGACAGAGAGA CTCTCTGTGATATCAAGAGAGA	248 249
Intron 21	A(+1)563 G	Not applicable	Allele 1: Allele 2:	CATCTAGGGATCATAGCCAT CATCTAGGGATCATAGCCAT	250 251
Intron 24	G(+1)321 T	Not applicable	Allele 1: Allele 2:	AAGTACAGTGGAGGAGACAGCG AAGTACAGTGGAGGAGACAGCG	252 253
Intron 29	A(-)1624 G	Not applicable	Allele 1: Allele 2:	AATTCCTAAAATAAGTAATGCA ATTCCTAAAATAAGTAATGCA	254 255
Intron 31	T(+1)30 C	Not applicable	More common: Less common:	GGCCCTGCCCTTATTATTACT GGCCCTGCCCTTATTATTACT	256 257
Intron 33	A(+1)732 G	Not applicable	Allele 1: Allele 2:	TGAGAGAAATTACTGACCCCG TGAGAGAAATTCTGACCCCG	258 259
Intron 33	C(+1)898 T	Not applicable	Allele 1: Allele 2:	TTTCTGAAACATCACTGCA TTTCTGAAATATATCTGAC	260 261
Intron 34	C(+1) 234 T	Not applicable	Allele 1: Allele 2:	AACCTCAGTTCCCTCATCTGNG AACCTCAGTTCCCTCATCTGNG	262 263
34	G4834A	R158TK	More common: Less common:	CTGGACACCAAGAAATATGTC CTGGACACCAAGAAATATGTC	264 265
37	C 5266G	S1731C	More common: Less common:	TCCTATGTGTCTCCACCAAT TCCTATGTGTCTCCACCAAT	266 267
Intron 43	T(+1)18 C	Not applicable	More common: Less common:	AAGAAGTGGCTGTATTTTGC AAGAAGTGGCTGTATTTTGC	268 269
Intron 43	C(+1)1665 G	Not applicable	Allele 1: Allele 2:	AACCTGATTTGATTTGTTAGCTG AACCTGATTTGATTTGTTAGCTG	270 271
48	G6521T	no change	More common: Less common:	CAGGTCACCAACCCGACCTGA CAGGTCACCAACCCGACCTGA	272 273
Intron 10	(+)14 ins. T	Not applicable	More common: Less common:	GGTCAGGATGCGGACAG GGTCAGGATGCGGACAG	284 285
Exon 16	G2547A	Y8251	More common: Less common:	CCACTCCGATCTCCATG CCACTCCGATCTCCATG	286 287
Polymorphism in an ABC1 PAC contig: This polymorphism is within approximately 200kb of the ABC1 gene					
A or G	Not applicable		Allele 1: Allele 2:	TTGGAGGCTAAGCCAGGAGAA TTGGAGGCTAAGCCAGGAGAA	274 275
					SEQ ID NO:

Figure 11D

Genomic contig containing ABC1 exon 1:

Underline = putative promoter element

acctcttatagaatgatagaattcctctggaatgattggataaacttcatttcaccttgacttttaccttggaggattt
 cttaccccttttggcttctcaaatttgactattaaaatgttgctttaaaaataggaacacagtttcaggggggagtag
 cageccatgacccttctgcaaggccccctaactcaaggtagttccctggaactgtggtttatggaatgtttcaggagt
 gtgaggaggtataatttaaggctgtcctagcaaggatacccttaaggatagagggccagtagcatctggaggccagaa
 aagttaaactgaggcagtcagattagcttcaggctcaattaagctgatgggtcagcctgggagaaattgcaggatgact
 ctcaatatccccctcccacccccacagcagccagatctgtctgtctttaatcatgggtgcagtgaacctgttcttcca
 ggtgtcttggccttcagtaacctgttaggctgtccctgaacgtggctaccgatccaaagacacatgatcagagagggc
 aattagagaacagaccttttccaaagcaagcatgttctgttgggttagaagtttcatgtcctaataattataggacct
 gtgcatctctctggagatgaggcacatgagtcataatctgtgattcttgccttttgtgtcaacatctcatgaataggcaat
 cagagctttggcaccatgtattttcagttcataatctgtatgttagttaaattccacctcctgctttgtagttaactggcaa
 gctgtttttgatataagacatctagaacactgtaaatatataacatttttatttgtctattataacctcaattacgaaaa
 agacatctagaagcaacctcatcaagagagatactgagggcgggcatggtagctcacacttgcaatcccattactttgg
 gaggctgaggcaggtagatcacttgaggtcaagagtttgaaccagcctggccaacatgttgaaacctgtctctatta
 aaaatacaaaaaagtttagctgggcttgggtgggtgggcacctgtaatcccagctactccggaggctgaggcaggagaaatca
 cttgaacctgggaggcagaggttgcagtgagctgagatcacaccactgcactccaacctgggcaccagagtgagattac
 atctaaaaataaaaaaagtaataaaaaagagagatattgatagctgttgttggaaatttcaacttccatctcacttc
 tggtaactttttggaagtttgttgaacaaagtggaaatcacgcacatacacacacatactctcttgtttgtttaa
 ggtttaatgaaatagctgtcatataatcactgttttgaagaggagaatttagttgctatctgtacattttgggtatgt
 gaactatttggatagaactctgagaaatgcattcagaacaacaaacaaatcataggagaaatagctaagtgggaaggg
 gcataaagagttgttgaaaaagttatttcttgagaacacagctctaattgctaggcaagtcacttgctttgggggaggc
 ctgagcttctctgtctataagattgcagcaggggtgtagtgggaatgagtcctcaacattccaagagattttatctact
 aatacgacagtcacaaatggagcatgactttgttgggaagcctctcctcttccaccagaggggccaatttctctgtcccagt
 gagatgttgacacttgtatgatccctgcttggagacttccctcttctggaacctgccctgggtcaggcatgagggtga
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 cccatttgttactgcacaagcaaacagcttctggtagctgtacagatacatgcactttcttctcactgtgtttccat
 agacagatttagtgctgtagaagtagagggcagtcacgggaaggagttcctgttttcttttggctatgccaaatgg
 ggaaaaatcctcctatcttctgtctttttagtgtcatcctctctccccttttcttctctttataattctcctctcatc
 tctcctggaaatgtgcatgtcaagttcaaaagggcacaatgttttggtaggaagggtgggagaaacacgtgccagggtg
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 tegtcaatcctaccaccaccaccactgtttgaacaaccactattatttgtctgtttcccatccctggtagaatagga
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 gaactcgataaaatatttgttgggtcatgggcaccttgacaggttaaggctgcagttgtttgtggaatttataagtg
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 tccaagttatgacttgtgaggtatgttaattatgataatagaaggcagtttatttgggtcagatttattgatgtgta
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 tttgggattcatccaggttgcgcatgtaacagtagcttattcctttttatggctgagtaagtgtcccagttttatttta
 tatattttatagaggaggtgtctcactctgtcaccaggtgagtgcggtagcgcgcatctcagctcactgcaacct
 ccgcctcccaggttcaagcaatttctcctgctcctgagtagtggtattacaggcaccaccgcccacgcccactaatt
 tttatatttttagtagagatggggttccaccatgttggcaggctgatctcaaactcttgacctcaggtgatccgccc
 cctctgggtcccaaagtgttaggattacaggcatgagccactgtgcccagccccagttttatttattcaccagttgatg
 gtcttttcgacaactaattgtttccagtttttggctattctgtataaggcttctataaatattcacaataacctaggat
 gggatgactgggtcatataatagtagtataaccttagcagaaactgtcaaactattttccaaagtggctcttccatt
 ttacaattccacagtgatttagtcccagtgctccatacacatgtagcacttttaataattttagtgggtatgt
 aatgatatctcattgtgttttaatttgcatttctctgcagctaattgatgagtggttctgtctatttgggaagggttta
 atttagcagtcgtgtgtattctgtatagataataaacttcaaaatatcagtggtcatttgcagttaaaatttctttaa
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 attttggcaaggagtgatccacttgggtgactgatgagaccagagagcgtacgcctcggggtgaggggtgaggacggg
 cggaagtgcactgcagtgccctgtgtggccttgggagggtgcccagtccttagctaaagctggcagttatgggaacag

Figure 12A-(1)

[illegible]

Figure 12A-(2)

gagggaggggaaggaagctgtgttggttttcacacagggattgatggaatctggctcttatggacacagaactgtgtggt
ccggatatggcatgtggcttatcatagagggcagatttgcagccaggtagaaatagtagcttttggtttgtgctactgcc
caggcatgagttctgatccctaggacctggctccgaatcgccccctgagcaccctcttttcttttggctgcagccctg
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gacgtcagctctttgtctctctatctctgaacacccttcttagagatcccatctctaggatgcatttctctgtagtta
gtttctaagctcttctgttctgttctgcctttatttttttctggattctaagccagtatccccacttggctgtctt
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tccgccatggtttatccatgttgtgtgtccattagtgagtagtggaagaatcatatcatgttggaatgaaagggggg
ctatggctctggggtagtctagctgaactcttatttt

Figure 12A-(3)

SEQ ID NO: 15

Genomic contig containing ABC1 exon 2:

[illegible]

Figure 12B - (1)

actggagtagcacaggaggagggttctagctcaggctgagatthtttagtaaaggaaattatgccacgatgaatcctgaag
aatgaatagaagtgaaccagataaagcacgataggaagcatcttcccttacctaagggaagacacagaggatatatggaat
ggtatgtttaaagggtgggactccaaacagttctgttaaagcttagagagtgggtgggagagactggagaagttgattaat
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atcttatttcccactcagTGTGAGCTGCTGCTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATCTCTGTTTCG
GCTGAGCTACCCACCTATGAACAACATGAATgtaagtaactgtggatggtgcctgagactcaccaatggcagggaaaat
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aacctagggttctaatthttgttgataaggcatgaactcaggagactgttttcagtcctagtgaatgggtgataattgtaatt
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attaaaagcacatttaagataatgccttaacacctagtctthttccatatgcatgatgtcttaatcacacattgcaaatca
tggaacacagaatttht

Figure 12B - (2)

SEO ID NO 16

Genomic contig containing ABC1 exon 3:

[illegible]

Figure 12C - (1)

cagggtttcgccatgttggccagggtggtcttgaactcctgacctcaggtgatccgcccaccttggcctcccaaagtgct
gggattacagggcgagccactgtgcccagcccacttcaccttaccgtagttacctccttagagtatgaaaaataggct
tagggcatccccaagtccctctatgtctgagagctgaggctggctgtcaaagaggaactaaggatgccagggaactttct
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acagacttggcatgaagcattgtataaatggagcctcaaaatcgcttcagggaattaatgtttctccctgtgttttcta
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GTAATGCCAACAACCCCTGTTTCCGTTACCCGACTCCTGGGGAGGCTCCCGGAGTTGTTGGAAACTTTAACAAATCCATg
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atggaccctagactggctttgtagcctccatgggccccttccatacac

Figure 12C - (2)

SEQ ID NO 17**Genomic contig containing ABC1 exon 4:**

tcatgactgccattggtataaagatgaatataatccagaccagattcatgattattcatacatttttagtgtattaactt
ttaattctgctttttaaataaaattaaaacattctaataatgcccttaagagtatcccagcccaggccactgagcctactgt
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gccagtaatggcatgt

Figure 12D

SEQ ID NO 18

Genomic contig containing ABC1 exon 5:

[illegible]

Figure 12E

SEQ ID NO 19**Genomic contig containing ABC1 exon 6:**

agtaaaatggagaattccaaattctgaaattgtagaacatagttctgtgtcttagttaaatatcgacacttacagataa
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Figure 12F

SEQ ID NO 20

Genomic contig containing ABC1 exon 8:

ccggtttggcaaatgctcagtaaaagaaaaggggttagaaggggagaaaggcattttatcccaagccttcaggaatcaggat
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Figure 12G - (1)

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Figure 12G - (2)

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Figure 12G - (3)

SEQ ID NO 21

Genomic contig containing ABC1 exon 9 through 22:

[illegible]

Figure 12H - (1)

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Figure 12H - (2)

[illegible]

Figure 12H - (3)

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Figure 12H - (4)

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Figure 12H - (5)

[illegible]

Figure 12H - (6)

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SEQ ID NO: 22
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Figure 12 I - (1)

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 caggctccattgcttcccagctgccaagaatgccttgggtgcagcacagtcattagggcctgcattcctcattggcgtgctg
 gttggctggggaggtgggctggactcgtagggtttggcccttggccttgtttctaacacttgcggttctctgctgtccc
 cctgccccctccactgcctgggtaaagATTGTCTTGCCAGCTGTGTTGTCTGCATTGCCCTTGTGTTTCAGCCTGATCGT
 GCCACCTTTGGCAAGTACCCAGCCTGGAACCTTCAGCCCTGGATGTACAACGAACAGTACACATTTGTCTCAGgtatgttt
 gtcttctacatcccaggagggggaagattcgagcagaccaaagatgttttacgagggccaagggaatggacttcagaatt
 acacggtggaat

Figure 12 I - (2)

SEQ ID NO: 23

Genomic contig containing ABC1 exon 29:

[illegible]

Figure 12J:

SEQ ID NO: 24

Genomic contig containing ABC1 exon 30 and 31:

tcttgccagtctctactcatttttcagcacatcgagcataagatccagactctttcccaggcctctctcatctggctcct
 ctctctctctttatcattactcttcttcgtagcttatctactccagccatgctgtcttcttattattcctaaaaarta
 gaaatgcatttcttcttagggcctttgtacctgcacttgccatcgcttttgctcagaatgttctttttgccaaagcttttg
 ccagcttggttctccatcattgttatgttttggtgaaatgttcttctcttagtaggttcattctccccagtcactgtctt
 tttattttgctttattttgggcatctaagggtatcttattagtgtatttggttgcgtctctccatgggcatacacct
 ccatgaaggcaggtattttcaccttagggcctcgaatatactggacagcatctggcacgtagtagatgctcaacgaatgt
 ttggtgtgtgagcaaatggttggttgattggattgaactgagttcagtagtaaatatttagggcctctttgcattctat
 tttacttatgtataaaatgatacataatgatgatataaatgatgtcacagtgtaacaggctgttggtggatcaagcaatc
 aaatgagatcatgcttgtcttttccaaatggtgagggaaatagatgcatgtttgtggttggttacggaatgatcctgtgtc
 ctgaggcaacagaaaggccaggccatctctggaatcctactcttgcgtcttccctttgcagAGACACGCCCTGCCAGG
 CAGGGGAGGAAGAGTGGACCACTGCCCCAGTTCCCCAGACCATCATGGACCTCTTCCAGAATGGGAACGGACAATGCAG
 AACCTTCACCTGCATGCCAGTGTAGCAGCGACAAAATCAAGAAGATGCTGCCCTGTGTGTCCCCCAGGGGAGGGGGCT
 GCCTCTCCACAgtgagtcactttcagggggtgattgggcagaaggggtgcaggatgggctggtagcttccgcttggaa
 gcaggaatgagtgagatatcatgttgggaggggtctgtttcagtcctttttgttttttttttctgaggcgaggct
 ttgctctgtcgccaggctggagtgctgtggcatgatcttgcctcactgcaacctccacctcccaggttcaagcgattct
 cctgcctcagcctcctgagtagctgggattacaggcagcgaccaccatgtctggctaatttttgtgttttttagtagagat
 aggggttctgcctgttggctaggctggtctggaattcctgacctcaggtgatccaccgcctcggcctcccaaagtgtctg
 ggattacaggcgtagccactacgcccagccctgtttcagtccttaactcgcttcttgcataagaaaaagcatgtgagt
 tttgaggggagaaggtttggaccacactgtgcccagcctgttcccacagcagtaaaagtcacaggacagactgtggcaggc
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 caggtgcgggggtggtcacacctgtaatctcagtagttttgggatgccgaggtggactgatcacctaagggtcaggagttcg
 aaaccagcttggccaatgtggcgaaaccctgtctctactaaaaaattcaaaaattagccaggcatggtggcacatgcctgt
 aatcccagttacttgggaggctgaagcaggagaattgcttgaacctgggaggtggaggtcgaggagccaaaattgcgc
 cactgtactccagcctgagcaacacagcaaaactccatatcaaaaaataaaaatgaataaaataacagctaattctagtc
 cagtataactccagtgaacagaagatttattaggcatagtgaatgatggtgcttcttaaaaaatctcttgactacaaagaa
 tctcatttcaatgtttattgttttagatgttcagaataaattcttgggaagaccttggcttgggtgtaagtgaattaccag
 tgccgagggcagggtgaaccaagtctcagtgctggttgactgagggcagtgctggtgacctgtagtcagggtttccggtca
 cactgtggacatggtcactgttgccttgatttgttttctgtttcaattcttgtctataaagacccgtatgcttgggttt
 catgtgatgacagAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCCGATTATCTGGTGA
 AGACGTATGTGCAGATCATAGCCAAAAGgtgactttttactaaacttggccctgccttattattactaattagaggaat
 taaagacctacaaataacagactgaaacagtgggggaaatgccagattatggcctgattctgtctattggaagtttagga
 tattatcccaactagaaaagatgacgagaggggactgtgaacattcagttgtcagcttcaaggctgaggcagcctgggtct
 agaatgaaaatagaaatggattcaacgtcaaattttggccac

Figure 12K

SEQ ID NO: 25

Genomic contig containing ABC1 exon 32: _

gcatgctggagtgatagtgaccatgagtttctaagaaagaagcataatctctccatattgtcatccacaattgaaatatta
ttgttaattgaaaaagcttctagggccaggcacgggtggctcatgcctgtaatcccagcactttaggagccaaggcgggtgg
atcacttgagggtcaggagtttgagaccagcctggccaacatggggaaccctgtctctactaaaaatacaaaaataagctg
ggcgtgggtgggtgcgtgcctgtaatcccagctacttgggaggctgaggcaggagaactgcttgaatctgggaggcggaggt
tgcagtgagctgagttcatgccattgcattccagcctgggcaacaagagcgaaaccatctcccaaagaaaaaaaaaaga
aagaaaaagcttctagtttggttacatcttggtctataagggtggtttgtaaattggtttaaccaaggcctggttctcat
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aaggccagctgattctagggtatattctgtccgttccttatatcctcaggtggatatttactccttttgcattcattagga
ataggctcagtgccttctttgaactgattttttgtttctttgtctctgcagCTTAAAGAACAAGATCTGGGTGAATGAGT
TTAGgtaagttgctgtctttctggcacgttttagctcagggggaggatggtgtttaggtgtgcttggttgaagaagcc
ttggggattgtttgtcactcacacacttggtgggtgccatctcactgtgagga

Figure 12L

SEQ ID NO: 26

Genomic contig containing ABC1 exon 33 to 36:

gctttatagagtttctgcctagagcatcatggctcagtgcccagcagccctccagaggcctctgaatatttgatatact
 gatttccttgaggagaatcagaaatctcctgcaggtgtctagggatttcaagtaagtagtggttgagggaatacctac
 ttgtactttcccccaaacagattccccagggtctcttaaggactcaaggacaatttctagggcatttagcacgggactaa
 aaaggtcttagaggaaataagaagcgccaaaaccatctctttgcactgtatttcaaccatttgccttctgggttttga
 aggaacaggtgggactggggacagaagagttcttgaagccagtttgtccatcatggaaaatgagataggtgatgtggcta
 cgtcagggggccgaaggctccttgttactgatttccgtcttttctctgccttttccccaggggccaggaccctgga
 tctctgggcagagcagacgcaggccccctataatagccctcatgctagaaaggagccggagcctgtgtataaggccagcgc
 agcctactctggacagtgcagggttcccactctcccaactccccatctgcttgcctccagaccacattcacacacgagc
 cactgggttggaggagcatctgtgagatgaaacaccattctttcctcaatgtctcagctatctaactgtgtgtgtaatca
 ggccaggtcctccctgctgggcagaaaccatgggagtttaagagattgccaacatttatttagaggaagctgacgtgtaact
 tctgaggcaaaatttagccctcctttgaacaggaatttgactcagtgaacctgtacacactcgactgagctgtgtgtgt
 gatgatactgtgcacccactgtctgggttttaatgtcaggtgttcttttagGTATGGCGGCTTTTCCCTGGGTGTCAG
 TAATACTCAAGCACTTCCTCCGAGTCAAGAAGTTAATGATGCCATCAAACAAATGAAGAAACACCTAAAGCTGGCCAAGG
 taaaatatctatcgtaagatgtatcagaaaaatgggcatgtagctgctgggatataggagtagttggcaggttaaaccgga
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 gaattacttagttgtacgttttaaagtgtaggtcaaaaacaaatccagaggccaggagctgtgggtcatgcctgtaatcc
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 caaaactccatctcaaaaaacaaattaaatccagagattttaaagctctcagaggctgggcgcggtgggttacacctgtt
 atcccagcattttgggatgccgaggcgggcaaagcacaaaggtcaggagtttgagaccagcctggccaacatagtgaacc
 ctgtctctgctaaaaacatagaaaaattagccgggcatgggtggcgtgcgcctgtaatcccagctactcgggaggctgagg
 tgagagaatttctgaacccgggaggcggaggttgagtgagccagattgcaccactgcactccagcctgggcgacaga
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 acatactttgctgaayaatcactgactaaataggaatgaatcttttttttttttttaagctggcaagctggtctg
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 catcactgctgtagatttctagtcacttgggttctcaggagccgtttatttaattggcttcacatttaatttcagtgaacaa
 ggtagtggcattgctcttcacaggggcgtcctgttgtccacaggttcagattgactgttggcccttatctatgtgaaca
 gtcacaactgaggcaggtttctgttgtttacagGACAGTTCTGCAGATCGATTCTCAACAGCTTGGGAAGATTATGAC
 AGGACTGGACACCAGAAATAATGTCAAGGtaaacccgtgtctttgttctagtagctttttgatgaacaataatccttatg
 tttcctggagtactttcaactcatggtaaaagtggcaggggcattcacacagaaaaagagcaaaactattaactttaccag
 tgaggcagtagcgtgtagtgtatgattcagagaatttgccttggcaccagacataccaggtaaccttgactaagttact
 taacctatctaaacctcagttycctcatctgtgaaatggagacagtaatcatagctatttccaaactgttgtgagaattc
 aatgagttaaaggtataaggtcctcaccacagcgcctgccacatagtcagtgatcactatgtcctgaacactgtaatta
 cttcgccatattctctgatcatagtgttttgccttgggtatgtgactagaatttcttctgaggtttatgggcatgggttg
 tgggtatgcacctgcctgcaggagccccggtttgggggcatcactgtacctgggtatgttttctttcagGTGTGGTTCAA
 TAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGAATGTTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAG
 AGAACCTAGCCATTATGGAATTACTGCTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGGCTCTg
 taagtgtggctgtgtctgtatagatggagtggggcaaggagaggggttatggagaaggggagaaaaatgtgaatctcatt
 gtagggaacagctgcagagaccgttatattatgataaatctggattgatccaggctctgggcagaagtgataagtttac
 gaattggctgggttgggcttcttgaactgcagaagagaaaatgacactgatatgtaaaatcgtaacatttagtgaattca

Figure 12M – (1)

tataaagtgagttcaaaaattgttaattaaattataatttaattataaagtgtttaatcagtttgatttggttataaaacca
 ctgttttaaaatttggtggaatatgtttttattagcttgatctttaattcctaaattaagctgtgtgtgtgtgtgtgtgt
 gtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgaagtttaagccaggatgagctagtttaagtatgcagcctttggagtc
 atacagatctgggtttgaatctggtctctaaactttatagatgtatgatattaaatgaggcagttcatgtaaattgccaa
 gcccagcactcagcacagagttgatatttcacacacattagatacctttcctgtatgtggagcatggcagttcctgtttc
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 gccagaaatattaattttatttgagtagttacagagtaaatatttctgctctcatttagttttcaagccccactagtccttt
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 CTCGTCGCCAGCCAGCTTTGTCTGATTCTCTGATCCAGGAGCGGGTCAGCAAAGCAAAACACCTGCAGTTCATCAGTGGAG
 TGAAGCCTGTCTACTGGCTCTCTAATTTTGTCTGGGATATGgttaaggacacaggcctgctgtatctttctgatgtct
 gtcaggggccatggattgatatggataaagaaagaaagagctctggctatcatcaggaaatgttccagctactctaaagatg
 tatgaaaaaagaatagccagaggcaggtgatcactttcatgacaccaaacacagcattgggtaccagagttcatgtcaca
 ccagagggaaaattctgtacacaatgatgaaaattaataccactaccacttaagttcctatgtgacaactttcccaagaa
 tcagagagatacaagtcaaaactccaagtcaatgcctctaacttctctgatgggttttaacctccagagtcagaatgttc
 tttgccttactaggaagccatctgtcatttagaaaactctgtacattttatcagcagcttatccatccattgcaaatat
 tgtttttgtgccasccacaatatattgcttctatttggaccaatatgggggatttgaaggaattctgaagttctaattat
 atttcaactctactttacaatatctccctgaaatatatctccctgtaacttctattaattataagctacacagagcaaat
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 agatctttgctgtttataccaagcccccttagactgtgtcactcttctgatccggttgccttgatggccatgctgtata
 ttgtgaatgtcccgttttcaaaagcaaagccaagaattaaccttgtgttcaggctgtggtctgaatgggttatgggtccag
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 aattctgacattcatgttatgagcagttacctcataaatagattacatg

Figure 12M – (2)

SEQ ID NO: 27

Genomic contig containing ABC1 exon 37 to 41:

aaattactctgactgggaatccatcggttcagtaagtttactgagtgtagacaccttggttgactggttgaaagacagaaa
 gggcatgtagttttataaaatcagccaaggggaaaatgcttggtcaaaatgtattgtcggttattttgattaatagtttatg
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 cattgtatatttgatttaggggtgaactggatgtctttgttttcacttttagTGCAATTACGTTGTCCCTGCCACACTGG
 TCATTATCATCTTCATCTGCTTCCAGCAGAAGTCTATGTGTCTCCACCAATCTGCCTGTGCTAGCCCTTCTACTTTTG
 CTGTATGGgtaagtcacctctgagtgagggagctgcacagtggtgataaggcatttggtgcccagtggtcagaaggaggcag
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 TCAAGATCCCCAGCACAGCCTATGTGGTGCTCACCAGCGTGAACCTCTTCATTGGCATTAAATGGCAGCGTGGCCACCTTT
 GTGCTGGAGCTGTTACCGACAATgtgagtcagtcagagagaacactcctgctgggatgagcatctctgggagccagagg
 acagtggttaattgtgatcttattccacttgtagtggtattgacactgctgactgccttgctcctgtcttcagagtcctgt
 cttccctgagaaggcaagcacctttctttcttgctgtgccttacattttgtctggtcaagcctttcagtttcttttgaca
 gttttttttacttctttcttttttcaatgttgctcttaccagagtagctcctctgccttccactttacacatgagagct
 gggcgacgcattcagtcctaaggcttttaccatcacctctcttggtgtttttattgtcatctctaagatcaatgccttta
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 actgggttatgttgtagtcttccaggtatggacctctaaaataaggcttccctctccattccgggtgtcattgcctttgt
 ccaaacacagcacacaaggccttttacagttgcacaactcttccgtgccataccaccacaccctttcccagctgtaagc
 ttcagatgagttgcctccaaccaccatgctcctgtaggcctggcttgaatgcccttctctgtcacaggggtctggtagt
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 aagggccatgggttttgatccctccattctgaccggatctctgcattgtgtctactagCGGAGAATCGCTTTGTGTCACC
 ATTATCTTGGGACTTGGTGGGACGAAACCTCTTCGCCATGGCCGTGGAAGGGTGGTGTCTTCTCATTACTGTTCTGA

Figure 12N – (1)

TCCAGTACAGATTCTTCATCAGGCCAGgtgagctttttcttagaaccctggagcacctgggtgaggggtcacagaggag
gcgcacagggaaacactcaccaatgggggttg cattgaactgaactcaaaatatgtgataaaactgattttcctgatgtg
ggcatcccgcagccccctccctgccatcctggagactgtggcaagtaggtttataatactacgttagagactgaatct
ttgtcctgaaaaatagtttgaaagggttcatttttcttggtttttcccccaagACCTGTAAATGCAAAGCTATCTCCTCTG
AATGATGAAGATGAAGATGTGAGGCGGGAAAGACAGAGAATTCTTGATGGTGGAGGCCAGAATGACATCTTAGAAATCAA
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tatatgcttacatttatgtgttagttattaaaacataactaatattgtatatctagtcaaactgagtagagagataatggt
gatt

Figure 12N – (2)

SEQ ID NO: 28

Genomic contig containing ABC1 exon 42 to 45:

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 ggttgcccagattgcgctgctgcactccagcctggtgacagagtgagactcatgtcaacaacaaaaacagaaaaagcacg
 cacatctaaaacatgcttttgtgatccatttgggatggtgatgacattcaaatagtttttaaaaatagattttctcctt
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 tttcacacattaactttggcctcaacttgacaactcaataatatttataaatacagccacacttaaaatggtcccatta
 tgaaatacatatttaaatatctatacagatgtgttaaaaccaagaaaaatatttgattcttctctgatatttaagaattgaa
 ggtttgaggttagttacgtgttaggggcatttatattcatgttttttagagtttgcttatacaacttaattcttcttcttca
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 GAGGAGATGCTTTCTTAAACAAAATAGgtgagaaaagaagtggccttgatatttgcgtgcaaagactttgttttaattta
 tttaaagaaataggttggtattttttagttacagtggtatttttagagttcataaaaatggtgaaatatagtaaagggtaa
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 tttacagcttttattcaggtataatttacatacaatataatttgccttggttttttaagagtataatttagtgatttttggg
 aaattgagagttttgcaaccatcaccacaatccagttttagaacttttccatcacccacatctgtcttatatacacata
 taaatgtgccatacaattgagatcatactgtatgtagaatttaaaatagtttttattgttaatgagtgatttatgaata
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Figure 120 – (1)

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Figure 120 – (2)

SEQ ID NO: 29

Genomic contig containing ABC1 exon 46 to 49:

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 ttataataatgacctgtttacaaatgaatttgaaagttactctaattctttgattcatcaagaaataactagaatggca
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Figure 12P – (1)

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Figure 12P – (2)

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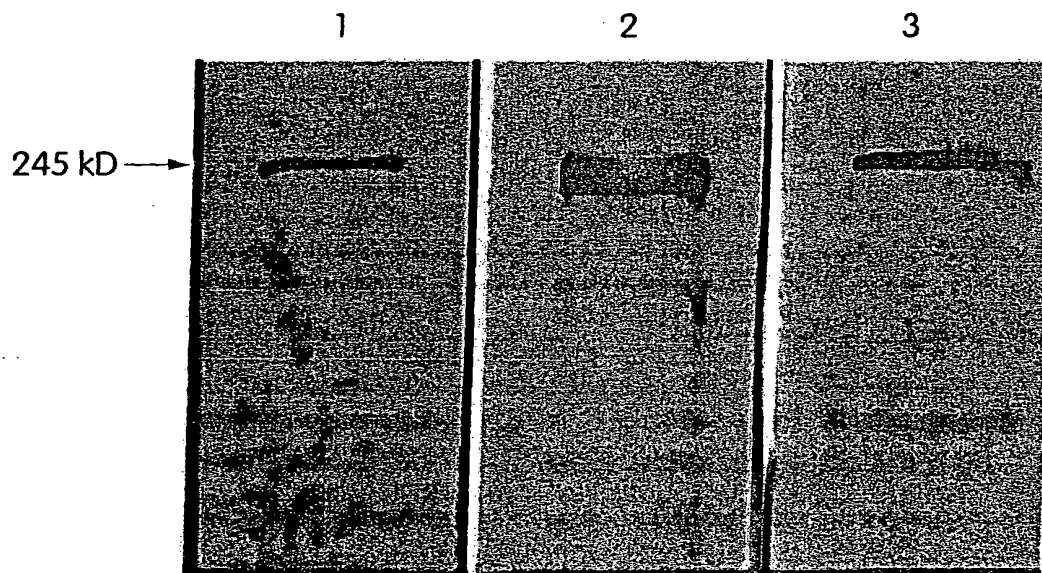
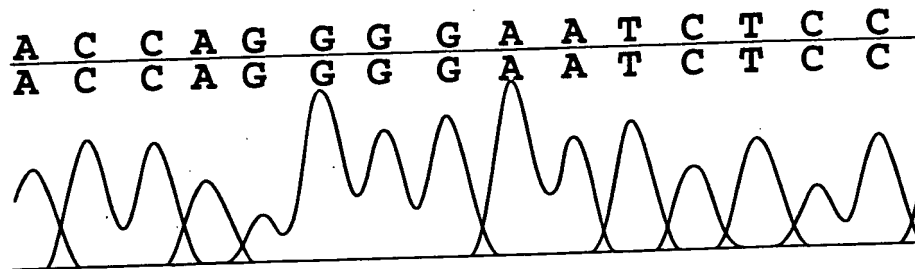


Fig. 13

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Control



WHAM

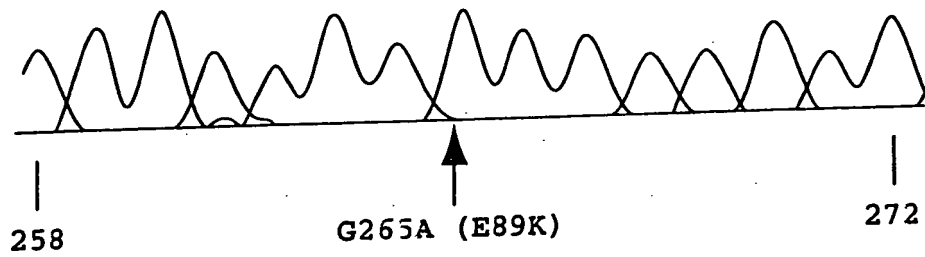
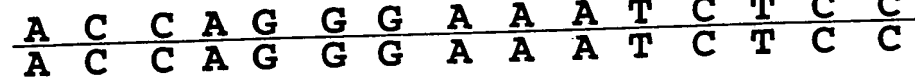


Fig. 14

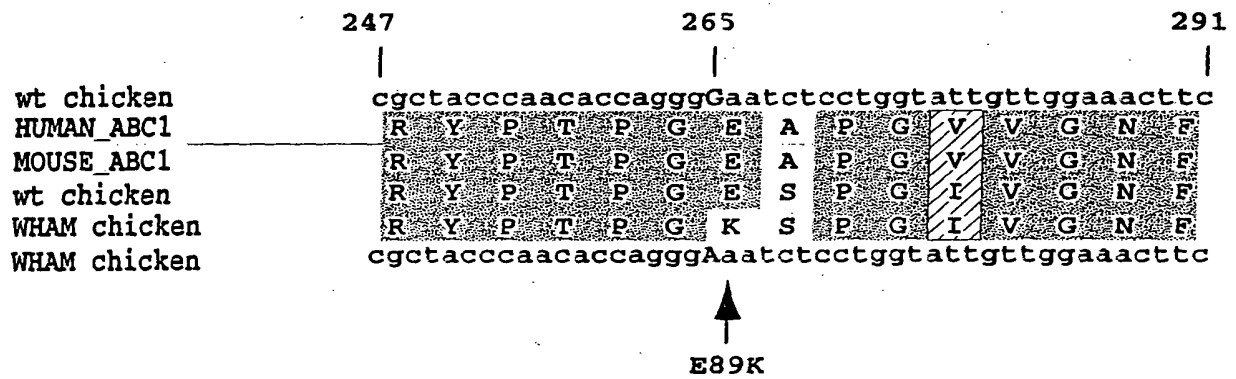


Fig. 15

No. Name	Location in SEQ ID No. 14	Sequence	Sequence Strand Length
1 PPRE	58-69	AGGTAAAGTCA	12 Complement
2 PPRE	1997-2009	AGAGTAGAGGGCA	13 Lead
3 PPRE	2150-2161	ATGTCAAGTCA	12 Lead
4 PPRE	2156-2169	AGTTCAAAAGGGCA	14 Lead
5 PPRE	4128-4139	AGGCAGCAGGGCC	14 Complement
6 PPRE	5075-5087	AGGCAGAGTGA	13 Lead
7 PPRE	6604-6615	ATGCCAAGGTCA	12 Complement
8 PPRE	6721-6743	GGGCGAAGGTA	13 Complement
9 PPRE	7220-7233	AGTAATGAGACA	14 Complement
10 PPRE	7554-7568	GGATCAGAGGTCA	15 Complement
1 SRE	159-166	CAGCCCAT	8 Lead
2 SRE	1133-1140	CAGCTCAC	8 Complement
3 SRE	1145-1152	CACACCAC	8 Lead
4 SRE	1809-1816	CAGCCCTC	8 Complement
5 SRE	1894-1901	CAGCCCAT	8 Lead
6 SRE	2563-2570	CAACCCAC	8 Lead
7 SRE	3303-3310	CAGCTCAC	8 Lead
8 SRE	3470-3477	CCGCCAC	8 Lead
9 SRE	4784-4791	CTCCCCAC	8 Lead
10 SRE	4802-4809	CAGCTTAC	8 Complement
11 SRE	4970-4977	CAGCTCAC	8 Complement
12 SRE	6487-6494	CAGCTTAC	8 Complement
13 SRE	6565-6572	CACCCAAC	8 Complement
14 SRE	6727-6734	CACCTCA	8 Lead
15 SRE	7041-7048	CACCCAAC	8 Lead
16 SRE	8059-8066	CAGCCCTC	8 Complement
1 ROR (retinoic acid receptor related)	166-172	AGGTCA	7 Complement
2 ROR (retinoic acid receptor related)	166-173	AGGGTCA	8 Complement
3 ROR (retinoic acid receptor related)	263-370	ATGGGTCA	8 Lead
4 ROR (retinoic acid receptor related)	264-370	TGGGTCA	7 Lead
5 ROR (retinoic acid receptor related)	228-2225	TAGGGTCA	8 Lead
6 ROR (retinoic acid receptor related)	2219-2225	AGGTCA	7 Lead
7 ROR (retinoic acid receptor related)	3643-2649	TGGGTCA	7 Lead
8 ROR (retinoic acid receptor related)	6604-6610	AGGTCA	7 Complement
1 SREBP-1 or "E box"	473-479	ACACCTG	7 Complement
2 SREBP-1 or "E box"	536-541	ACACATG	7 Lead
3 SREBP-1 or "E box"	537-543	TCATGTG	7 Complement
4 SREBP-1 or "E box"	655-661	TCATGTG	7 Complement
5 SREBP-1 or "E box"	925-931	ACACTTG	7 Lead
6 SREBP-1 or "E box"	967-973	TCACTTG	7 Lead
7 SREBP-1 or "E box"	968-974	TCAAGTG	7 Complement
8 SREBP-1 or "E box"	1033-1069	ACAGGTG	7 Complement
9 SREBP-1 or "E box"	1104-1110	TCAGTTG	7 Lead
10 SREBP-1 or "E box"	1105-1111	TCAAGTG	7 Complement
11 SREBP-1 or "E box"	1561-1567	TCACTTG	7 Lead

Figure 16A

12	SREBP-1	or	"E box"	1670-1676	TCAATG	7	Lead
13	SREBP-1	or	"E box"	1748-1754	ACAATG	7	Lead
14	SREBP-1	or	"E box"	1749-1755	ACAATG	7	Complement
15	SREBP-1	or	"E box"	1852-1858	TCATGTG	7	Lead
16	SREBP-1	or	"E box"	1853-1859	ACACATG	7	Complement
17	SREBP-1	or	"E box"	1899-1905	ACAAATG	7	Complement
18	SREBP-1	or	"E box"	2199-2205	ACACGTG	7	Lead
19	SREBP-1	or	"E box"	2393-2399	ACACGTG	7	Complement
20	SREBP-1	or	"E box"	2669-27005	ACACCTG	7	Lead
21	SREBP-1	or	"E box"	2677-2683	TCACATG	7	Complement
22	SREBP-1	or	"E box"	2740-2746	ACAATG	7	Complement
23	SREBP-1	or	"E box"	2969-2975	ACAATG	7	Complement
24	SREBP-1	or	"E box"	2979-2985	ACACATG	7	Lead
25	SREBP-1	or	"E box"	2981-2987	ACATGTG	7	Lead
26	SREBP-1	or	"E box"	2980-2986	ACATGTG	7	Lead
27	SREBP-1	or	"E box"	2982-2988	ACATGTG	7	Complement
28	SREBP-1	or	"E box"	3461-3467	ACACATG	7	Complement
29	SREBP-1	or	"E box"	3462-2468	TCACCTG	7	Lead
30	SREBP-1	or	"E box"	3547-3553	TCAACTG	7	Complement
31	SREBP-1	or	"E box"	3752-3758	ACACATG	7	Complement
32	SREBP-1	or	"E box"	4226-4232	TCACCTG	7	Lead
33	SREBP-1	or	"E box"	4582-4588	ACACGTG	7	Lead
34	SREBP-1	or	"E box"	4588-4594	TCAGTTG	7	Complement
35	SREBP-1	or	"E box"	4861-4867	TCAGGTG	7	Lead
36	SREBP-1	or	"E box"	4951-4957	ACAATG	7	Lead
37	SREBP-1	or	"E box"	5096-5102	TCAATG	7	Complement
38	SREBP-1	or	"E box"	5912-5918	ACAGTTG	7	Lead
39	SREBP-1	or	"E box"	5913-5919	TCAACTG	7	Complement
40	SREBP-1	or	"E box"	6245-6251	ACACATG	7	Complement
41	SREBP-1	or	"E box"	6288-6294	ACAATG	7	Complement
42	SREBP-1	or	"E box"	6623-6629	TCATTTG	7	Lead
43	SREBP-1	or	"E box"	6836-6842	TCACCTG	7	Lead
44	SREBP-1	or	"E box"	6837-6843	ACAGGTG	7	Complement
45	SREBP-1	or	"E box"	7032-7038	ACAGGTG	7	Complement
46	SREBP-1	or	"E box"	7069-7075	TCAGGTG	7	Lead
47	SREBP-1	or	"E box"	7101-7107	ACATATG	7	Complement
48	SREBP-1	or	"E box"	7138-7144	ACAGTTG	7	Lead
49	SREBP-1	or	"E box"	7139-7145	TCAACTG	7	Complement
50	SREBP-1	or	"E box"	7240-7246	ACACCTG	7	Complement
51	SREBP-1	or	"E box"	7467-7473	ACAGGTG	7	Lead
52	SREBP-1	or	"E box"	7640-7646	TCATTTG	7	Lead
53	SREBP-1	or	"E box"	7641-7647	TCAATG	7	Complement
54	SREBP-1	or	"E box"	7653-7659	TCAGTTG	7	Lead
55	SREBP-1	or	"E box"	7654-7660	ACAATG	7	Complement
56	SREBP-1	or	"E box"	7735-7741	ACAATG	7	Lead
57	SREBP-1	or	"E box"	7838-7844	TCAGGTG	7	Complement
58	SREBP-1	or	"E box"	7880-7886	TCATCTG	7	Complement
59	SREBP-1	or	"E box"	8051-8057	TCAGCTG	7	Lead
60	SREBP-1	or	"E box"	8052-8058	TCAGCTG	7	Complement

Figure 16B